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                                            rattus norv
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rhodobacter
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022137; CA142686.1; -; Genomic_DNA.
GO; GO:0004815; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0006464; P:protein modification; IEA.
InterPro; IRR004344; Tub_tyr_lygase.
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al Similarity 100.0%; Pred. No. 0;
390; Conservative 0; Mismatches
                                                                                | 0.583R8 EMENI | 0.8583R8 EMENI | 0.8583R EMENS | 0.96030 HUMAN | 0.574 M HUMAN | 0.95441 HUMAN | 0.746P8 THETE | 0.53405 FARUM | 0.34721 SEPHIN | 0.34721 SEP
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                    GA45A MOUSE
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    01010000000000
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NUCLEOTIDE SEQUENCE
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  NCBI_TaxID=9606;
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(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                 May 15, 2006, 09:56:51; Search time 91 Seconds
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                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4930524K07 product:hypothetical Tubulin-tyrosine ligase
containing protein, full insert sequence.
                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUB=Testis;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                              Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                        518 AA
                 QLNAHPLEPVLRGLKTAEGALRPPBGGKGS 747
QLNAHPLEPVLRGLKTAEGALRPPPGGKGS
                                                                                                                                                                                                                                                                                          Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL/6J; TISSUE-Testis;
The FANTOM Consortium,
                                                                                                     QECOV2 MOUSE PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001)
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                                                                                                                                                                                                                                               Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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512
                              718
                                                                                          MOUSE
                                                                          RESULT
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01-MAR-2003 (TrENBLrel. 23, Last sequence update)
01-MAR-2004 (TrENBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933401B17 product:hypothetical Tubulin-tyrosine ligase
containing protein, full insert sequence.
Name=1700019P01Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6J; TISSUB=Testis;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hizaka T., Hirozane T., Hayatshida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Shiraki T., Sogabe Y., Tagami M., Tagawa D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Tagami Comaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Fuguri A., Ohle D., Ohle D., Muramatsu M., Hayashizaki Y., Fuguri A., Full College M., Muramatsu M., Hayashizaki Y., Fuguri A., Full College M., Full College M., Hayashizaki Y., Fuguri A., Full College M., Full College M., Full College M., Hayashizaki Y., Fuguri A., Full College M., Full College 
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatu M., Inoue Y., Kira A., Hayashizaki Y., Rixen integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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Pred. No. 9.1e-42;
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Pfam, PF03133; Ttl, 1.
Hypothetical protein; Ligase.
SEQUENCE 518 AA; 59319 MW; 540C045659FACOD6 CRC64;
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Ensembl; ENSMUSG0000022388; Mus musculus.
MGI; MGI:1922902; 1700019P01Rik.
GQ; GQ:0016874; F:ligase activity; IEA.
GQ; GQ:0004835; F:tubulin-tyrosine ligase ac
GQ; GO:000464; P:protein modification; IEA.
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Q8CON7;
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Q96GG8 HUMAN
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobri T., Bono H., Kasukawa T., Saito R., D. Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Makell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whishaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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R. Submitted (Jul-2001) to the EMBL/GenBank/DobJ databases.

R. Binsembl; Ramulsono0000022388; Mus musculus.

R. GO; GO:0016874; F:ligase activity; IEA.

R. GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.

R. GO; GO:00048464; P:protein modification; IEA.

InterPro; IPR000276; GPCR Rhodpsn.

InterPro; IPR004344; Tub_tyr_ligase.
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STRAIN=C57BL/6J; TISSUB=Testis;

MEDLINE=2059013; PUDMed=1107661; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Aumin V., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rikki integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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TISSUE=Testis;

MIDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A District R.F., Jordan H., Moore T., Max S. I., Wang J., Heiseh F.,

District R.F., Jordan H., Moore T., Max S. I., Wang J., Heiseh F.,

A District R.F., Jordan H., Moore T., Max S. I., Wang J., Heiseh F.,

A Cappleton M., Soares M.B., Bonaldo M.F., Carvinci P., Prange C.,

Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Robert S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaraenne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Warley D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Shakesley W., Touchman J.W., Schen E.D., Dickson M.C.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Schnerch A., Schein J.E., J.M., Marra M.A.,

Schnerch A., Schein J.E., Schutter B.D., Schutter H.D., Schutter 
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Name=RGD1306462_predicted;
Name=RGD1306462_predicted;
Rattus norvegicus (Ratl).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchoncoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                         395 DTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN
                                                                                                                                                                                                                                                     192 DIKFDIROWFLVTDWNPLTIWFYKESYLRFSTORFSLDKLDSAIHLCNN
                                                                                                                                       Length 781;
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Pred. No. 2.4e-09;
                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, BC097453, AAH97453.1; -; mRNA.
InterPro; IPR000276; GPCR_Rhodpsn.
PROSITE; PS00237; G PROTEIN RECEP F1 1; UNKNOWN 1.
SEQUENCE 375 AA; 72908 MW; 566FBÄl19C61BEIF_CRC64;
Pfam; PF03133; TTL; 1.
PROSTITE; PS00237; G PROTEIN RECEP_F1_1; UNKNOWN_1.
Hypothetical protein; Ligase.
Hypothetical protein; Ligase.
T81 AA; 89398 MW; 9E98793C3351C3DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                    9.1%; Score 49; DB 2; L. 100.0%; Pred. No. 1.3e-41; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 ACKVCQAYLGQLEHEDID 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
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                                                                                                                            Ouery Match
Best Local Similarity 100.0
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Q4V8C1 RAT PRELIMINARY;
Q4V8C1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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rissum=Pooled;
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SEQUENCE
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                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (UUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC009479; AAH09479.11; -; mRNA. GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:0006464; P:protein modification; IEA. InterProx. IPRO04344; Tub_tyr_lygase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03133; TTL; 1. -
SEQUENCE 101 AA; 12054 MW; BEACD6C1131E0DF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Tubulin tyrosine ligase-like family, member 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                        Last sequence update)
Last annotation update)
101 AA.
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                                                                        Created)
   PRT;
                                                                    01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 ROWFLVTDWNPLT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 ROWFLVTDWNPLT 78
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QSect2;
   Q96GG8 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
                                                                                                                                                                         TTLL3 protein.
Name=TTLL3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
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MEDINE-2238827; PubMed-1247932; DOI=10.1073/pnas.242603899;
MEDINE-2238827; PubMed-1247932; DOI=10.1073/pnas.242603899;
A Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
A Hakeeley R.W., Touchman J.W., Garen E.D., Dickson M.C.,
A Blakeeley R.W., Touchman J.W., Garen E.D., Dickson M.C.,
A Schmerch A., Schein J.B., Jones S.J.M., Marra M.A.,
B Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,

R Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101; Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T., Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L., Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G., Perrea G., Holt I., Karamycheva S., Liang F., Quackenbush J., Keele J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        T.P.L.;
                                                                                                                                                                                              "Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle."; Genome Res. 11:626-630(2001).
                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Pooled,
Harhay G.P., Sonstegard T.S., Van Tassell C.P., Clawson M.L.,
Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.
"Sequencing and analysis of Bos taurus full-length insert cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13; DB 2; Length 261;
Pred. No. 0.00031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 AA; 29911 MW; 5F069784CA162017 CRC64;
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Last sequence update)
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1... 0; Mismatches
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NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BT021865; AAX46712.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 ROWFLVTDWNPLT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 ROWFLVTDWNPLT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q922T0 MOUSE PRELIMINARY;
Q922T0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
hes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4833441J24Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=4833441J24Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                     The German cDNA Consortium;
198 ROWFLVTDWNPLT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGAWA3_HUMAN PRELIMINARY;
QGAWA3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q4KMS8 HUMAN PRELIMINARY;
Q4KMS8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
des 13; Conservative
                                                                                                                                                                                                                                                              Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Cervix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=TTLL3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
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                                                                                    RESULT 9
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                                                                                                  Q6AWA3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Fetal liver;
Yu Y., Zhang C., Luo L., Ouyang S., Zhang S., Li W., Wu J., Zhou S.,
Liu M., He F.;
Functional prediction of the coding sequences of 50 new genes deduced
by analysis of cDNA clones from human fetal liver.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 TTL domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                2.4%; Score 13; DB 2; Length 266; 100.0%; Pred. No. 0.00031; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.4%; Score 13; DB 1; Length 352; .00.0%; Pred. No. 0.0004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                    EMBL, BC006830; AAH06830.1; -; mRNA.
Ensembl; ENSMUSG00003030276; Mus musculus.
MGI: MGI: 2141418; MGI: 2141418; MGI: MGI: 2141418; Etubulin-tyrosine ligase activity; IEA.
GO; GO:0006464; P:protein modification; IEA.
InterPro; IPR004344; Tub_tyr_ligase.
Pfam; PF03131; TTL; SEQUENCE 266 AA; 30506 MW; F8EBFB52FA8B8E98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
    Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 290 M -> R (in dbSNP:2290305).

/ FTTd=VAR 020207.

67 67 I -> F (in Ref. 2).

352 AA; 40356 MW; 49FDBEB118C7C20D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 61-352.
                                                                                                                                                                                                                                                                                                                                                                                                                 TTLL3 HUMAN STANDARD; PRT; 352 AA. 0974AF, Q9U199; CEFEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Tubulin tyrosine ligase-like protein 3 (HOTTL) Name=TTLL3; ORFNames=PRO0207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensembl; ENSG0000156983; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL096725; CAB46375.1; -; mRNA.
EMBL; AF078842; AAF23353.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC; HGNC:24483; TTLL3.
InterPro; IPR004344; Tub_tyr_ligase.
Pfam; PF03133; TTL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The German cDNA consortium;
                                                                                                                                                                                                                                                                              198 ROWFLVTDWNPLT 210
                                                                                                                                                                                                                                                                                                       66 RQWFLVTDWNPLT 78
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les 13; Conservative
                                                                                                                                                                                                                                         13, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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Matches
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MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
R Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
R Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Perange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, BK48175; CAH10554.1; -; mRNA.
GO, GO:00046435; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:000464; P:protein modification; IEA.
InterPro: IRR04434; Tub_tyr_lygase.
Pfam, PF03133; TTL; 1.
Hypothetical protein.
SEQUENCE 352 AA; 40257 MW; 49FD8E9CAEICB20D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nowo saprems (namam).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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100.0%; Pred. No. 0.0004;
cive 0; Mismatches 0; Indels
                                                                                                                                                                   Last sequence update)
Last annotation update)
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13.SEP-2005 (TrEMBLrel. 31, Last sequence update)
13.SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (TTLL3 protein).
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PRT;
                                                                                                            Created)
                                                                                                                                                                                                                                                    Hypothetical protein DKFZp686D076.
Name=DKFZp686D076;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                            126 RQWFLVTDWNPLT 138
                                                                                                                                                                                                                                                                                                       198 ROWFLVTDWNPLT 210
                                                  rescued clones;
                                                                                                                                                                                                                                                                                                                                                                                                               Q4RY08 TETNG PRELIMINARY;
Q4RY08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 431:946-957(2004).
                                                                                                                                                                                                                                         Query Match 2.45
Best Local Similarity 100.0
Matches 13; Conservative
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nes 13; Conserv
                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                             434 AA;
                                                TISSUE=PCR rescue
                                                                                                                                                                                                             SEQUENCE
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        ð
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XX MEDLINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

XI RIAUSHOR R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Batchenco M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA A. McCharde S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Notlalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Nitialon D.K., Muzny D.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schuntz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

B Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

B A Mannan A.M. Schein J.E., Jones S.J.M., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                       ö
   Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S., submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                   Score 13; DB 2; Length 352;
Pred. No. 0.0004;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                            NIH MGC Project;
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC099361; AAH98361.1; -; mRNA.
EMBL; BC099735; AAH99735.1; -; mRNA.
Hypothetical protein.
SEQUENCE 352 AA; 40381 MW; 49EF0C1118C7DD12 CRC64;
                                                                                                                                                                 NIH MGC Project;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein DKFZp586B0320.
                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 AA.
                                                                                                                                                                                                                                                                                                                                             2.4%; Sco...
100.0%; Pred. No. v...
'... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      198 ROWFLVTDWNPLT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 ROWFLVTDWNPLT 138
                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
TISSUE=PCR rescued clones;
                                                                                                                                  NUCLEOTIDE SEQUENCE.
TISSUE=PCR rescued clones;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBNDN8 HUMAN PRELIMINARY;
QBNDN8;
                                                                                                                                                                                                                                                                                                                                                   2.47
Best Local Similarity 100.0
Matches 13; Conservative
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Authoria Seguena N.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 0.00059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.4%; Score 13; DB 2; Length 434; 100.0%; Pred. No. 0.00049; ive 0; Mismatches 0; Indels
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Submitted (100-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL83393; CAD38794.1; -; mRNA. EMBL; BC098298; AAH98298.1; -; mRNA. GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:0006464; P:protein modification; IEA. Interbro; IRR004344; Tub.tyr_ligase. Feam; PF03133; TTL; 1.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 11 SCAF14979, whole genome shotgun sequence.
ORFNames=GSTENG00027209001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
EMBL; CAAE01014979; CAG06724.1; -; Genomic DNA.
SEQUENCE 534 AA; 60130 MW; 62B5BBBB696B662B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         49433 MW; 9E79E6CA08651CA1 CRC64;
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100.0%; Pred. No. v..
.. 0; Mismatches
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mouse cDNA sequences."

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Query Match
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g
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUB=Thymus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                           STRAIN=CS7BL/6J; TISSUE=Thymus; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashlzaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                           01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
library, clone:A633053H17 product:HOTTL PROTEIN homolog.
Name=4833441J34Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
                                   PRT;
                                                      Created)
                                  QBBV51_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001)
                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                                                                                 NCBI_TaxID=10090;
                                                     01-MAR-2003
                        MOUSE
                RESULT 13
                        08BV51
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TISSUB-INVIOL GLOUGH COLOUR T., Sugiyama T., Irie R.,
TACLEDID SUZUKI Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
TA Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
Yamamoto J.-I., Sato K., Kawai Y., Isono Y., Nakamura Y.,
Nagahari K., Yasuda T., Isono Y., Nakamura Y.,
Nagahari K., Yasuda T., Iwayanagi T., Wagatsuma M.,
Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
Omura Y., Abe K., Kamihara K., Yasuta M., Sato K., Tanikawa M.,
Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
Pujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
Rusano J., Kanehori K., Takahashi-Pujii A., Hara H., Tanase T.-O.,
Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
Nomura Y., Musashino K., Yuuki H., Oshima A., Sasaki N., Satok S.,
Yoshikawa Y., Matsumawa H., Ichihara R., Sasaki N., Sauki O.,
Nomiyama H., Satoh N., Takami S., Tarashima Y., Suzuki O.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport of the control of the cont
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-184-format sequencing pipeline with 384 multicapillary sequencer.";
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 0.00075;
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13; Conservative 0; Mismatches
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Q9H876;
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NUCLEOTIDE SEQUENCE
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Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hizao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komateu T., Mizuno J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Mizubiima Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Nakai K., Yada T., Nomura Y., Ohara O., Isogai T., Sugano S., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Ucomplete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Anophales gambiae Sequence Committee,
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Genet. 36:40-45(2004).
EMBL, AK023960, BAB14'41.1; -; MRNA.
Ensembl, ENSG00000156893; Homo sapiens.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0006484; P:tubulin-tyrosine ligase activity; IEA.
InterPro; IPR004344; Tub_tyr_lygase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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EMBL; AAAB01008980; EAA13905.2; -; Genomic_DNA.

GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA

GO; GO:0006464; P:protein modification; IEA.

InterPro; IFR06344; Tub_tyr_lygase.

Pfam; PF03133; TTL; 1.
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744 AA; 84683 MW; DF661753E4AFFODF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            572
67109 MW; 8938D9EDD5935071 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANCO0000022337 (Fragment).
ORFNames=ENSANGG0000019848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          572 AA.
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The Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 ROWFLVTDWNPLT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROWFLVTDWNPLT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 ANOGA
Q7Q156 ANOGA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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NCBL_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004344; Tr
Pfam; PF03133; TTL; 1.
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Best Local Similarity
Thes 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
NUCLEOTIDE SEQUENCE.
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SEQUENCE
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Length 572;

2.2%; Score 12; DB 2; 100.0%; Pred. No. 0.007;

Query Match Best Local Similarity

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

May 15, 2006, 09:57:43 ; Search time 17 Seconds Run on:

(without alignments) 3061.957 Million cell updates/sec

US-10-635-977-2 541 1 MASSILKWVVSHQSCSRSSR......LRGLKTAEGALRPPFGGKGS 541 Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283416 segs, 96216763 residues Searched:

Word size :

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR 80:* Database :

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	13	2.4	352	. 7	T12515	hypothetical prote
7	9	1.7	547	7	AI0990	methyl-accepting c
m	6	1.7	547	~	A47178	methyl-accepting t
4	80	1.5	110	~	D82628	hypothetical prote
Ŋ	8	1.5	165	7	B56535	DNA-damage-inducib
9	80	1.5	264	~	JC5640	2-hydroxypent-2,4-
7	80	1.5	269	~	E95999	probable methyl-tr
89	8	1.5	325	~	G87447	conserved hypothet
6	8	1.5	453	7	867089	hypothetical prote
10	80	1.5	503	~	S21805	portal protein - p
11	8	1.5	513	~	A87324	hypothetical prote
12	80	1.5	533	7	T26860	
13	ω	1.5	557	7	T41495	hypothetical prote
14	80	1.5	830	7	F83288	ω
15	7	1.3	74	7	157554	interleukin-3 rece
16	7	1.3	92	7	S52277	hypothetical prote
17	7	1.3	113	8	A75626	salicylate monooxy
18	7	1.3	124	7	S20545	phosphate acceptor
19	7	1.3	130	Н	HSRT2A	histone H2A - rat
20	7	1.3	142	~	JS0510	fusaric acid resis
21	7	1.3	144	7	F97044	
22	7	1.3	162	Н	Z3BPL7	gene 3 protein - p
23	7	1.3	162	Н	Z3BP22	protein -
24	7	1.3		~	F75253	conserved hypothet
25	7	1.3	-	~	T06250	probable resistanc
56	7	1.3		~	AG0687	tail core protein
27	7	1.3	188	~	C87487	ribosome recycling
28	7	1.3	199	~	149745	HMG box protein -
29	7	1.3	205	~	B95285	conserved hypothet

2 H83619 hypothetical	2 C85499 hypothetical		1 QRECFH ferrichrome transp		2 I40886 glycine hydroxymet	2 E81395 indole-3-glycerol	2 E75493 hypothetical prote	2 A70113 methionine aminope	2 G83959 tRNA methyltransfe	F69725	2 G97425 Flagellar L-ring	AG2643	F75121	2 T07755 disease resistance	0
270	265	265	265	262	260	258	253	251	246	243	239	239	229	227	223
1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3
45 7	44 7	43 7	42 7	41 7	40 7	39 7	38 7	37 7	36 7	35 7	34 7	33 7	32 7	31 7	30 7
7	7 1.3 265 2 (265 2 (7 1.3 265 1	7 1.3 262 2 TO5654	260 2 I40886	258 2 E81395	253 2	251 2	246 2 (243 2	239 2	239 2	229 2	227 2	7

ALIGNMENTS

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RESULT 1
T12515
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Archard protein DKFZp434B103.1 - human C.Species: Home sapiens (man) C.Species: Jul-1999 #text_change 09-Jul-2004 C.Accession: T12515
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. Spinnitted to the Protein Sequence Database, June 1999
A;Reference number: Z17524
A;Accession: T12515
A;Accession: T12515
A;Accession: T12515
A;Accession: T12515
A;Residues: J.352 < WAM>
A;Residues: J.SS2 < WAM>
A;Residues

Gaps ö 2.4%; Score 13; DB 2; Length 352; 100.0%; Pred. No. 0.00011; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 13; Conservative

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198 ROWFLVTDWNPLT 210

126 RQWFLVTDWNPLT 138

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RESULT 2
A10990
methyl-accepting chemotaxis citrate transducer [imported] - Salmonella enterica subsp.
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001
C;Accession: A10990
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, t., T.; Connerton, P.; Croin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Authors: preliminary
A;Accession: A10990
A;Accession: A10990
A;Accession: A10990
A;Accession: L547 cPAR>
A;Residues: 1-547 cPAR>
A;Residues: 1-547 cPAR>
A;Residues: 1-547 cPAR>
A;Coss-references: UNIPARC:UPI000005A77D; GB:AL513382; PIDN:CAD08053.1; PID:gl6505033; C;Genetics:
A;Gene: STY4234
C;Superfamily: methyl-accepting chemotaxis protein

Length 547; Query Match 1.7%; Score 9; DB 2; Best Local Similarity 100.0%; Pred. No. 1.8; 2

```
Mb. damped inducible protein gadd45 - mouse
Ny.Alternate names: MyD18 protein homolog
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: B55535; 149679
R;Zhan, Q; Lord, K.A.; Alamo Jr., I.; Hollander, M.C.; Carrier, F.; Ron, D.; Kohn, K.W Mol. Cell. Biol. 14, 2361-2371, 1994
A;Title: The gadd and MyD genes define a novel set of mammalian genes encoding acidic payReference number: A56535; MUID:94187707; PMID:8139541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: UNIPROT: P48316, UNIPARC:UP1000001902, GB:L28177, NID:g456100; PIDN R;Alimzhanov, M.B.; Kuprash, D.V.; Turetskaya, R.L.; Osipovich, O.A.; Borodulina, O.R.; Borodulina, O.R.; Borodulina, O.R.; Borodulina, O.R.; Borlina, D.Y.; Turetskaya, R.L.; Osipovich, O.A.; Borodulina, O.R.; Borlina, D.R.; A;Title: Cloning and characterisics of murine genes coding for the human GADD45 analog A;Reference number: 149679; MUID:94154610; PMID:7509226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: 149679
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-165 <RES>
A,Cross-references: UNIPARC:UPI0000001902; EMBL:U00937; NID:g392933; PIDN:AAC27351.1; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kim, S.; Kweon, O.K.; Kim, Y.; Kim, C.K.; Lee, K.S.; Kim, Y.C.
Biochem. Biophys. Res. Commun. 238, 56-60, 1997
A;Title: Localization and sequence analysis of the phnH gene encoding 2-hydroxypent-2,4
A;Reference number: JC5640; MUID:97445124; PMID:9299451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1.264 <KLMA
A;Residues: 1.264 <KLMA
A;Cross-references: UNIPROT:034721; UNIPARC:UPI00000BA64D; GB:U97697; NID:g2316025; PID:
A;Experimental source: strain DJ77
C;Comment: This enzyme is responsible for the conversion of 2-hydroxypent-2,4-dienoate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Species: Pseudomonas sp.
C,Date: 27-Oct-1997 #sequence_revision 27-Oct-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2-hydroxypent-2,4-dienoate hydratase (EC 4.2.1.-) - Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 15/2; 49/2; 128/3
C;Superfamily: human DNA-damage-inducible protein gadd45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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C;Superfamily: 2-hydroxypenta-2,4-dienoate hydratase
C;Keywords: carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.5%; Score 8; DB 2;
100.0%; Pred. No. 10;
iive 0; Mismatches
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100.0%; Pred. No. 6.9
ive 0; Mismatches
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Matches 8; Conservative
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Matches 8; Conservative
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                               445
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A;Molecule type: DNA
A;Residues: 1-165 <ZHA>
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                            438
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A;Experimental source: strain 9a5c

B;Simpson, A.J.G.; Reinard, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

Bibmitted to Genbank, June 2000

A;Authors: Ferreira, W.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigt A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Martins, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; R.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Aluthors: da Silva, A.C.R.; da Silva, A.M.; Salvaak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvairi, A.M.; Verfore, A.L.; A.M.; A.C.R.; A.M.; Salvairi, A.M.; Verfore, A.L.; A.M.; Reference number: AS9328
                                                                                                                                                                                                                                                                                                                                                                                                                               R;Yamamoto, K.; Imae, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 217-221, 1993
A;Title: Cloning and characterization of the Salmonella typhimurium-specific chemorecept
A;Reference number: A47178; MUID:93126346; PMID:8419927
A;Accession: A47178
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-547 </MA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82628
C;Accession: D82628
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                               methyl-accepting transmembrane citrate/phenol chemoreceptor Tcp - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: UNIPROT:Q02755; UNIPARC:UP1000012EDAA; GB:L06029; NID:g154380; PIDN
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A; Experimental source: ST1
A; Note: sequence extracted from NCBI backbone (NCBIN:122070, NCBIP:122071)
C; Superfamily: methyl-accepting chemotaxis protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Gaps
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Mismatches
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Conservative
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Tue May 16 10:49:04 2006

N;Alternate names: hypothetical protein 04814

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C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 31-Dec-2004
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A,Cross-references: SGD:S0005723
A,Map position: 158
C,Superfamily: Metacaspase
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                          C; Species: Sinorhizobium meliloti
C; Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 12-Jul-2004
C; Joate: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 12-Jul-2004
C; Accession: E95999
R; Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A; Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A; Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                   A, Cross-references: UNIPROT: Q92U77; UNIPARC: UPI0000004790; GB:AL591985; PIDN: CAC49661.1; A, Cross-references: UNIPROT: Q92U77; UNIPARC: UPI0000004790; GB:AL591985; PIDN: CAC49661.1; A; Experimental source: strain 1021, megaplasmid pSymB R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001 A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A; Reference number: A96039; MUID:21368234; PMID:11474104
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C;Species: Caulobacter crescentus
C;Date: 20.Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87447
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Lamb, M.T.; DeBoy, R.T.; Dodson, R.J.; Dodson, R.J.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A,Residues: 1-325 <STO>
A,Cross-references: UNIPROT:Q9A7W9; UNIPARC:UPI00000C7438; GB:AE005673; NID:g13422997;
                                                                                  probable methyl-transferase, S-Adenosyl-L-methionine (SAM)-MTase protein [imported]
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100.0%; Pred. No. 12;
ive 0; Mismatches
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100.0%; Pred. No. 10.
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Pred. No. 10;
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Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-269 <KUR>
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A;Gene: SMb21433
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A;Gene: CC1600
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A;Molecule type: DNA
A;Residues: 1-432 «HUG»
A;Cross-references: UNIPROT:008601; UNIPARC:UPI0000698BA; EMBL:Z75105; NID:g1420468; P1
A;Experimental source: strain S288C
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Cispecies: phage SPP1
Cipate: 12-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
CiAccession: 821805; 824455; 744270; 836725
R;Tavares, P.; Santos, M.A.; Lurz, R.; Morelli, G.; de Lencastre, H.; Trautner, T.A.
A;Title: Identification of a gene in Bacillus subtilis bacteriophage SPP1 determining ti
A;Reference number: $21805; MUID:92260540; PMID:1583695
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A; Residues: 1-503 <TAX>
A; Cross-schences: 1-503 <TAX>
A; Cross-schences: 1-503 <TAX>
Cross-schences: UNIPROT: P54309; UNIPARC: UPI00001359D0; EMBL: X56064; NID: 915464; PIDP
B; Chai, S.; Bravo, A.; Lueder, G.; Nedlin, A.; Trautner, T.A.; Alonso, J.C.
J. Mol. Biol. 224, 87-102, 1992
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A; Residues: 1-37 < CHA>.
A; Cross-schences: UnIPARC: UPI000017A851; EMBL: X56064
A; Cross-chences: UNIPARC: UPI000017A851; EMBL: X56064
B; Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
Gene 204, 201-212, 1997
A; Title: The complete nucleotide sequence and functional organization of Bacillus subtil
A; Reference number: 222137; MUID: 98094274; PMID: 9434185
A; Accession: T42270
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A;Cross-references: UNIPARC:UPI00001359D0; EMBL:X97918; PIDN:CAA66580.1
C;Genetics:
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C,Accession: S67089
R,Hughes, B.; Pohl, T.M.
Squence Database, July 1996
A,Reference number: S66685
A,Accession: S67089
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A,Molecule type: DNA
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100.0%; Pred. No. 18;
iive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches
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Length 557;

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conserved hypothetical protein PA2858 [imported] - Pseudomonas aeruginosa (strain PAO1) C,Species: Pseudomonas aeruginosa (c,Species: Pseudomonas aeruginosa (c,Species: Pseudomonas aeruginosa (c,Species: D. Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 (c,Accession: P83288 R,Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim and a., Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
A,Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path A,Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path A,Title: DNA A,Refeatus: preliminary A,Molecule type: DNA A,Molecule type: DNA A,Molecule type: DNA A,Molecule type: L930 cSTO> A,Coss-references: UNIPROT:O9HZY6; UNIPARC:UPI00000C5849; GB:AE004712; GB:AE004091; NIA, Experimental source: strain PAO1
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R;Hannemann, J.; Hara, T.; Kawai, M.; Miyajima, A.; Ostertag, W.; Stocking, C.
R;Hannemann, J.; Hara, T.; Kawai, M.; Miyajima, A.; Ostertag, W.; Stocking, C.
A;Title: Sequential mutations in the interleukin-3 (IL3)/granulocyte-macrophage colony-mediated by a truncated beta C subunit.
A;Reference number: 157554; MUID:95257920; PMID:7739524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Mosecule type: mRNA
A;Mosecule type: mRNA
A;Kosidues: 1-74 «RES-
A;Cross-references: UNIPROT:Q64130; UNIPARC:UPI00000E599C; GB:S78451; NID:g998544; PIDN
C;Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor i
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C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: PA2858
C;Superfamily: Escherichia coli probable membrane protein ybbP
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100.0%; Pred. No. 36;
tive 0; Mismatches
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                           1.5%; Score 8; DB 2
100.0%; Pred. No. 19;
iive 0; Mismatches
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Job time : 19 secs
Query Match
Best Local Similarity 100..
دمو 8; Conservative
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Matches 7; Conservative
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B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, M.J.; Endlate, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Mittle: Complete Genome Sequence of Caulobacter crescentus.

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Scatus: prellminary

A;Scatus: prellminary

A;Residues: 1-S13 <STO>

A;Cross-references: UNIPROF:Q9AAJ4; UNIPARC:UPI00000C70DC; GB:AE005673; NID:g13421807; FC;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-533 <WILD>
A;Cross-references: UNIPROT:Q9XWX4; UNIPARC:UPI000007A7D5; EMBL:AL032623; PIDN:CAA21512.
A;Experimental source: clone Y43F8B
C;Genetics:
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A;Cross-references: UNIPROT:094602; UNIPARC:UPI00006A248; EMBL:AL033127; PIDN:CAA21871.
A;Experimental source: strain 972h-; cosmid c622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypotherical protein Y43F8B.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aare: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
C;Accession: T2686
R;Ainscough, R.
Submitted to the EMBL Data Library, October 1998
A;Reference number: Z20278
                                     C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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hypothetical protein CC0603 [imported] - Caulobacter crescentus
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A;Introns: 48/1; 100/3; 201/1; 257/2; 350/3; 483/3
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100.0%; Pred. No. 18;
tive 0; Mismatches
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Sequence 11159, A Sequence 16, Appl Sequence 30, Appl

Sequence

Sequence 2, Appliance 2, Appliance 23722, Appliance 23722, Appliance 23722, Appliance 23721, Appliance 237131, Appliance 21312, Appliance 23720, Appliance 2372

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APPLICANT: Wang, Xin Wei
APPLICANT: Wang, Xin Wei
APPLICANT: Harris, Curtis C.
APPLICANT: Fornacco Jr., Albert J.
APPLICANT: Coursen, Jill D.
APPLICANT: Zhan, Qimin
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
FILE REPERENCE: 015280-367100US
CURRENT APPLICATION NUMBER: US/11/297,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 113;
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                    1. US-11-087-099-11159
1. US-11-074-176-16
1. US-11-074-176-16
1. US-11-074-129-2
1. US-11-108-298-9222
1. US-11-188-298-17748
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1. US-11-188-298-7779
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1. US-11-096-568A-25774
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1. US-11-096-568A-16519
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TITLE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.5%; Score 8; DB 9
100.0%; Pred. No. 2.6
iive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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  , ORGANISM: human
US-10-784-004-1238
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US-11-297-160-8
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                                                                                                                                                                                                                             (without alignments)
488.448 Million cell updates/sec
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1 MASSILKWVVSHQSCSRSSR......LRGLKTAEGALRPPPGGKGS
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1: /SIDS5/ptodata/1/pubpaa/USOB_NEW_PUB.pepl:*
2: /SIDS5/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
6: /SIDS5/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
8: /SIDS5/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
9: /SIDS5/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
11: /SIDS5/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
11: /SIDS5/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
11: /SIDS5/ptodata/1/pubpaa/USII_NEW_PUB.pep:*
12: /SIDS5/ptodata/1/pubpaa/USII_NEW_PUB.pep:*
                                GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                May 15, 2006, 09:58:33 ; Search time 52 Seconds
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US-11-297-160-8
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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Query Match 1.5
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Albumin Fusion Proteins FILE REPERBURE: PF603 CURRENT APPLICATION WINDER: US/11/175,690 CURRENT APPLICATION WINDER: US/11/175,690 CURRENT FILING DATE: 2006-07-07 CURRENT FILING DATE: 2004-01-20 PRIOR APPLICATION NUMBER: US 60/441,305 PRIOR FILING DATE: 2003-01-20 PRIOR APPLICATION NUMBER: US 60/441,305 PRIOR PILING DATE: 2003-03-11 PRIOR PRELICATION NUMBER: US 60/472,816 PRIOR FILING DATE: 2003-03-11 PRIOR PRELICATION NUMBER: US 60/472,816 PRIOR FILING DATE: 2003-05-02 PRIOR PILING DATE: 2003-05-03 PRIOR PILING DATE: 2003-05-03 PRIOR PILING DATE: 2003-05-04 PRIOR PRIUNG DATE: 2003-05-04 PRIOR PILING DATE: 2003-05-04 PRIOR FILING DATE: 2003-05-04 PRIOR FILING DATE: 2003-05-06 PRIOR FILING DATE: 2003-05-04 PRIOR FILING DATE: 2003-05-04 PRIOR FILING DATE: 2003-05-04 PRIOR FILING DATE: 2003-09-30 PRIOR FILING DATE: 2003-09-30 PRIOR FILING DATE: 2003-09-30
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1.5%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 4.1
Matches 8; Conservative 0; Mismatches
CURRENT FILING DATE: 2005-12-07
PRIOR APPLICATION NUMBER: US/10/600,158
PRIOR FILING DATE: 2003-06-20
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,069
PRIOR APPLICATION NUMBER: US 60/126,069
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTH: 165
TYPE: PRT
CREATH: 165
TYPE: PRT
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US-11-175-690-345
; Sequence 345, Application US/11175690
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US-11-175-690-344
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SEQ ID NO 344
LENGTH: 181
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
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100.0%; Pred. No. 4.1;
1ve 0; Mismatches
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Publication No. US20060014254A1
GENERAL INFORMATION:
APPLICANT: Haseltine et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF605
CURRENT APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2005-07-07
PRIOR PELING DATE: 2004-01-20
PRIOR PELING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: US 60/441,305
PRIOR APPLICATION NUMBER: US 60/45,201
PRIOR APPLICATION NUMBER: US 60/45,201
PRIOR APPLICATION NUMBER: US 60/475,201
PRIOR PILING DATE: 2003-05-02
PRIOR FILING DATE: 2003-05-02
PRIOR PLING DATE: 2003-05-05
PRIOR PLING DATE: 2003-09-30
PRIOR FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: US 60/476,267
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/505,172
PRIOR PILING DATE: 2003-09-24
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 568
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 348
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 349
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US-11-175-690-349
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US-11-175-690-348
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Matches 8; Conserv
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                               DB 11; Length 181; 4.1;
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                            Query Match
1.5%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 4.1
Matches 8; Conservative 0; Mismatches
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PRIOR PELING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: PCT/USO4/001369
PRIOR PLILING DATE: 2004-01-22
PRIOR PLILING DATE: 2003-01-22
PRIOR PLILING DATE: 2003-01-12
PRIOR PLILING DATE: 2003-03-11
PRIOR PELICATION NUMBER: US 60/45,221
PRIOR PELING DATE: 2003-05-02
PRIOR PELING DATE: 2003-05-05
PRIOR PELING DATE: 2003-05-24
PRIOR PELING DATE: 2003-05-24
PRIOR PLILING DATE: 2003-05-24
PRIOR APPLICATION NUMBER: US 60/505,172
PRIOR PLILING DATE: 2003-09-24
PRIOR PLILING DATE: 2003-09-24
PRIOR PLILING DATE: 2003-09-30
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Publication No. US20060014254A1
GENERAL INFORMATION:
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REPRENCE: PF065
CURRENT APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2005-07-07
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CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: PCT/USO4/001369
PRIOR FILING DATE: 2004-01-20
PRIOR PLING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/451,305
PRIOR APPLICATION NUMBER: US 60/453,201
PRIOR PLING DATE: 2003-03-11
PRIOR PLING DATE: 2003-03-11
PRIOR PLING DATE: 2003-05-02
PRIOR PLING DATE: 2003-05-02
PRIOR PLING DATE: 2003-05-02
PRIOR PLING DATE: 2003-05-02
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; Sequence 348, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORWATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
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Pred. No.
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1.5%;
Best Local Similarity 100.0%;
Matches 8; Conservative 0
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US-11-175-690-347
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133 GALRPPPG 140
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US-11-175-690-347
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LENGTH: 181
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Query Match 1.5%; Score 8; DB 11; Length 790; Best Local Similarity 100.0%; Pred. No. 17;
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publication No. US200600142541
GENERAL INPORMATION:
APPLICANT: Haseltine et al.
TITLE OF INVENTION:
CURRENT PRILION Albumin Fusion Proteins
FILE REFERENCE: PF605
CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: US 60/441,305
PRIOR FILING DATE: 2003-01-22
PRIOR FILING DATE: 2003-01-11
PRIOR FILING DATE: 2003-03-01
PRIOR FILING DATE: 2003-03-01
PRIOR FILING DATE: 2003-05-05
PRIOR FILING DATE: 2003-05-05
PRIOR PRILING DATE: 2003-05-05
PRIOR PRILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US 60/476,267
PRIOR PRILING DATE: 2003-05-06
PRIOR PRILING DATE: 2003-05-06
PRIOR PRILING DATE: 2003-05-06
PRIOR PRILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR PRILING DATE: 2003-05-06
PRIOR PLING DATE: 2003-05-06
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100.0%; Pred. No. 17;
cive 0; Mismatches
                  TITLE OF INVENTION: Albumin Fusion Proteins
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
US-11-175-690-259
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ORGANISM: Homo sapiens
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US-11-175-690-259
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LENGTH: 790
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100.0%; Pred. No. 17;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            Length 261;
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1.5%; Score 8; DB 11;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches (
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FILE REFERENCE: PF605
CURRENT APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2005-07-07
PRIOR PELLON NUMBER: PCT/US04/001369
PRIOR FILING DATE: 2004-01-20
PRIOR FILING DATE: 2003-01-22
PRIOR FILING DATE: 2003-01-22
PRIOR FILING DATE: 2003-01-12
PRIOR FILING DATE: 2003-01-13
PRIOR FILING DATE: 2003-01-1
PRIOR FILING DATE: 2003-05-1
PRIOR FILING DATE: 2003-05-03
PRIOR FILING DATE: 2003-05-03
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 568
SOFTWARE: Patentin Ver: 2.0
LENTH: 790
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| LOCATION: (1).-(1261)
| PUTER INFORMATION: Ceres Seq. ID no. 12381376
US-11-096-568A-20320
  TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-155920632
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20320
LENGTH: 261
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US-11-175-690-258
; Sequence 258, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
, APPLICANT: Haseltine et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 257, Application US/11175690 Publication No. US20060014254A1 GENERAL INFORMATION:
                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays subsp. mays
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
US-11-175-690-257
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US-11-175-690-257
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APPLICANT: Haseltine et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF605
CURRENT APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: US 60/441,305
PRIOR FILING DATE: 2004-01-20
PRIOR PELICATION NUMBER: US 60/441,305
PRIOR FILING DATE: 2003-01-22
PRIOR PELICATION NUMBER: US 60/45,201
PRIOR PILING DATE: 2003-03-11
PRIOR FILING DATE: 2003-05-05
PRIOR PILING DATE: 2003-05-05
PRIOR PILING DATE: 2003-05-05
PRIOR PILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-05-04
PRIOR FILING DATE: 2003-05-04
PRIOR FILING DATE: 2003-05-04
PRIOR PILING DATE: 2003-05-04
PRIOR PILING DATE: 2003-09-30
NUMBER OF SED ID NOS: 568
SOFTWARE: PALENTIN VENER: US 60/506,746
PRIOR FILING DATE: 2003-09-30
NUMBER OF SED ID NOS: 568
SOFTWARE: PALENTIN VENER: US 60/506,746
SEQ ID NO 262
LENGTH: 790
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100.0%; Pred. No. 17;
iive 0; Mismatches
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1.5%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches
                              60/506,746
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PRIOR FILING DATE: 2003-09-24
PRIOR PELLING DATE: 2003-09-30
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 568
SOFTWARE: Patentin Ver. 2.0
LENGTH: 790
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
US-11-175-690-261
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US-11-175-690-262
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Publication No. US20060014254A1
GENERAL INFORMATION:
    TITLE OF INFORMATION:
    TITLE OF INVENTION: Albumin Fusion Proteins
    FILE REFERENCE: PF665
CURRENT APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2006-07-07
PRIOR APPLICATION NUMBER: US 60/441,305
PRIOR FILING DATE: 2003-01-22
PRIOR FILING DATE: 2003-01-22
PRIOR FILING DATE: 2003-01-12
PRIOR PELICATION NUMBER: US 60/467,222
PRIOR FILING DATE: 2003-05-01
PRIOR PILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US 60/472,816
PRIOR APPLICATION NUMBER: US 60/476,267
PRIOR APPLICATION NUMBER: US 60/476,267
PRIOR FILING DATE: 2003-05-23
PRIOR PILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 568
SOFTWARR: PALCATION NUMBER: US 60/506,746
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 568
SOFTWARR: PALCATION VUMBER: US 60/506,746
PRIOR APPLICATION NUMBER: US 60/506,746
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 568
SEQ ID NO 260
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Publication No. US20060014254A1
GENERAL INFORMATION:
APPLICANT: Haseltine et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF666
CURRENT APPLICATION NUMBER: US/11/175,690
CURRENT APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2005-07-07
PRIOR FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 60/441,305
PRIOR APPLICATION NUMBER: US 60/45,201
PRIOR APPLICATION NUMBER: US 60/45,201
PRIOR APPLICATION NUMBER: US 60/47,222
PRIOR FILING DATE: 2003-05-02
PRIOR FILING DATE: 2003-05-02
PRIOR FILING DATE: 2003-05-02
PRIOR FILING DATE: 2003-05-03
PRIOR FILING DATE: 2003-05-03
PRIOR FILING DATE: 2003-05-05
PRIOR FILING DATE: 2003-05-05
PRIOR PUBLICATION NUMBER: US 60/476,267
PRIOR PLING DATE: 2003-05-05
PRIOR PUBLICATION NUMBER: US 60/476,267
PRIOR PLING DATE: 2003-05-06
     Mismatches
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     8; Conservative
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; ORGANISM: Homo sapiens
US-11-175-690-260
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157 GALRPPPG 164
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Sequence 2, Application US/10615659
Publication No. US20040157234A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BG842
FILE REFERENCE: DO23 NP
CURRENT APPLICATION NUMBER: US/10/615,659
CURRENT FILING DATE: 2003-07-09
PRIOR PILING DATE: 2002-07-09
NUMBER: OF SEQ ID NOS: 102
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US-10-635-977-47
US-10-635-977-49
US-10-635-977-69
US-10-635-977-51
US-10-615-659-38
US-10-615-659-40
US-10-615-659-42
US-10-615-617-42
US-10-615-617-42
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Pred. No. 0;
); Mismatches
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SEQ ID NO 2
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       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-615-659-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
     541;
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Sequence 13, Application US/10615659
Publication No. US20040157234A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REFERENCE: DO283 NP
CURRENT APPLICATION NUMBER: US/10/615,659
CURRENT FILING DATE: 2003-07-09
PRIOR FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 102
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Sequence 2, Application US/10635977

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Publication No. US20040171131A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

FILE REPERENCE: D0283A CIP

CURRENT PAPLICATION NUMBER: U.S. 60/394,725

PRIOR FILING DATE: 2003-07-09

PRIOR FILING DATE: 2003-07-09

PRIOR FILING DATE: 2003-07-09

PRIOR FILING DATE: 2003-07-09

NUMBER OF SEQ ID NOS: 103

SOFTWARE: Patentin version 3.2

SEQ ID NOS: 103
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100.0%; Pred. No. 0;
:ive 0; Mismatches
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Matches 541; Conservative
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Sequence 14, Application US/10635977

Sequence 14, Application US/10635977

Sequence 14, Application US/10635977

Publication No. US20040171131A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: TRROSINE-LIKE PROTEIN, BGS42

FILE REFERENCE: D0283A CIP

CURRENT FILING DATE: 2003-08-07

PRIOR APPLICATION NUMBER: US. 60/394,725

PRIOR APPLICATION NUMBER: US. 10/615,659

PRIOR FILING DATE: 2003-07-09

NUMBER OF SEQ ID NOS: 103

SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                               Query Match 54.2%; Score 293; DB 4; Le Best Local Similarity 100.0%; Pred. No. 6.4e-287; Matches 293; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/615,659
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: U.S. 60/394,725
PRIOR FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIAN VERSION 3.2
SEGU ID NO 14
LENGTH: 293
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; ORGANISM: Homo sapiens
US-10-615-659-14
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                                           Sequence 13, Application US/10635977
Publication No. US20040171131A1
GENERAL INFORMATION:
TUTION OF US20040171131A1
APPLICANT: Bristol Myers Squibb Company
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
CURRENT PILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: U.S. 60/394,725
PRIOR APPLICATION NUMBER: U.S. 60/394,725
PRIOR APPLICATION NUMBER: U.S. 10/615,659
PRIOR FILING DATE: 2003-07-09
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Patentin version 3.2
SEQ ID NO 13
LENGTH: 541
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US-10-615-659-14

Sequence 14, Application US/10615659

Publication No. US20040157234A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

FILE REFERENCE: D0293 NP
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Sequence 21, Application US/10615659

Publication No. US20040157234A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

CURRENT APPLICATION NUMBER: US/10/615,659

CURRENT FILING DATE: 2003-07-09

PRIOR FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 102

SOFTWARE: Patentin version 3.2
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Sequence 22, Application US/2040157234A1
Publication No. US20040157234A1
GENERAL INFORMATION:
TITLE OF INVENTION: POLYNUCLEOTIDES ENCOING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REPERENCE: D0243 NP
CURRENT APPLICATION NUMBER: US/10/615,659
                                                                                                                                                                                                                                                                                                                                          193 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR 252
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                                                                                                                                                                                                                0; Indels
                                                                                                                                                                      44.7%; Score 242; DB 4; Le
100.0%; Pred. No. 1.9e-235;
tive 0; Mismatches 0;
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  NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 242
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                                                                                                                                                                                                                Matches 242; Conservative
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ORGANISM: Mus musculus
US-10-615-659-21
                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 49; Conservat
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Best Local Similarity
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US-10-615-659-22
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REFERENCE: D0283A CIP
CURRENT APPLICATION WUMBER: US/10/635,977
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: U.S. 60/394,725
PRIOR APPLICATION NUMBER: U.S. 10/615,659
PRIOR FILING DATE: 2003-07-09
                                                                                                                                                                                                                                                                                                                                                                                           ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDIGNFELLW 240
                                                                                          181 SPLLPAHNWWTSTRFQEYLQRQCRGAVWGSVIYPSWKKAIAHAMKVAQDHVEPRKNSFEL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR 120
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1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
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Publication No. US20040157234A1

GENERAL INFORMATION:

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS:

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS:

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

CURRENT APPLICATION NUMBER: US/10/615,659

CURRENT APPLICATION NUMBER: US. 60/394,725

PRIOR FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 102

SOFTWARE: Patentin version 3.2

LENGTH: 242
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100.0%; Pred. No. 1.9e-235;
tive 0; Mismatches 0;
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Publication No. US20040171131A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Best Local Simi
Matches 242;
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Sequence 24, Application US/10635977

Publication No. US20040171131A1

BUBLICAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

TITLE OF INVENTION: TO283A CIP

CURRENT APPLICATION NUMBER: US/10/635,977

CURRENT FILING DATE: 2003-08-07

PRIOR FILING DATE: 2002-07-09

PRIOR APPLICATION NUMBER: U.S. 60/394,725

PRIOR FILING DATE: 2003-07-09

PRIOR FILING DATE: 2003-07-09

PRIOR FILING DATE: 2003-07-09

NUMBER OF SEQ ID NOS: 103

SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/10615659
Publication No. US20040157234A1
ABBRIGANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
FILE REFERENCE: DO283 NP
CURRENT APPLICATION NUMBER: US/10/615,659
CURRENT FILING DATE: 2003-07-09
PRIOR FILING DATE: 2002-07-09
PRIOR FILING DATE: 2002-07-09
                                                                                                                                                                                                1 DTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN 49
                                                                                                                                                                      192 DIKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN
                                                               Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.8%; Score 42; DB 4; Length 42; Best Local Similarity 100.0%; Pred. No. 5e-34; Matches 42; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 5e-34;
ive 0; Mismatches 0; Indels
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                                                         Score 49; DB 4; L. Pred. No. 4.8e-41;
                                                         Query Match 9.1%; Score 49; DB Best Local Similarity 100.0%; Pred. No. 4.8 Matches 49; Conservative 0; Mismatches
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SOFTWARE: PatentIn version 3.2
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Best Local Similarity 100.0
Matches 42; Conservative
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US-10-615-659-24
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US-10-615-659-24
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US-10-635-977-24
        JS-10-635-977-22
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LENGTH: 42
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| Publication No. US20040171131A1
| GENERAL INFORMATION: US20040171131A1
| APPLICANT: Bristol-Myers Squibb Company
| TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
| TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
| TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
| FILE REFERENCE: D0283A CIP
| CURRENT FILING DATE: 2003-08-07
| FRIOR PRIOR FILING DATE: 2002-07-09
| FRIOR FILING DATE: 2002-07-09
| FRIOR FILING DATE: 2003-07-09
| NUMBER OF SEQ ID NOS: 103
| SOFTWARE: DatentIn version 3.2
| LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REFERENCE: DO283A CTP
CURRENT APPLICATION NUMBER: US/10/635,977
PRIOR APPLICATION NUMBER: U.S. 60/394,725
PRIOR APPLICATION NUMBER: U.S. 60/394,725
PRIOR FILING DATE: 2002-07-09
FRIOR APPLICATION NUMBER: U.S.10/615,659
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                       Query Match 9.1%; Score 49; DB 4; Length 49; Best Local Similarity 100.0%; Pred. No. 4.8e-41; Matches 49; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.8e-41;
tive 0; Mismatches 0; Indels
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: U.S. 60/394,725
PRIOR FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/10635977
Publication No. US20040171131A1
GENERAL INFORMATION:
                                                                                                                                                                                       TYPE: PRT

ORGANISM: Rattus norvegicus

US-10-615-659-22
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ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0
Matches 49; Conservative
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US-10-635-977-21
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US-10-635-977-22
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                                                                                                                                   SEQ ID NO 22
LENGTH: 49
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LENGTH: 49
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RESULT 15

US-10-615-659-23

US-10-615-659-23

i Sequence 23, Application US/10615659

i Publication No. US200401572441

i GENERAL INPORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

TITLE OF TILNED DATE: 2002-07-09

CURRENT APPLICATION NUMBER: US. 60/394,725

PRIOR APPLICATION NUMBER: US. 60/394,725

PRIOR APPLICATION NUMBER: US. 60/394,725

PRIOR SEQ ID NOS: 102

SOFTWARE: Parter of the company of the company of the company match of the company match of the company of the company of the company match of the company match
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Search completed: May 15, 2006, 09:59:56 Job time: 85 secs

Sequence 32, Appli Sequence 4, Appli Sequence 21551, A Sequence 746, App Sequence 26175, A Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 10, Appli

17, Appl 7125, Ap 34, Appl

Sequence 10, 8 Sequence 10, 8 Sequence 110, 8 Sequence 4125, 8 Sequence 4189, 8 Sequence 6280, 8 Sequence 880, 8 Sequence 880, 8 Sequence 880,

4499, Ap 6280, Ap 7316, Ap 880, App 880, App

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US-09-473-551-9

WG-09-473-551-9

Sequence 9, Application US/09473551

Sequence 9, Application US/09473551

GENERAL INFORMATION:

APPLICANT: MALDRANDT, Jeffrey D.

APPLICANT: MALOH, Robert H.

TITLE OF INVENTION: GFR-alpha-1-RET Specific Agonists and Methods Therefor

FILE REPERENCE: 6029-9879

CURRENT FILIG APPLICATION NUMBER: US/09/473,551

CURRENT FILIG APPLICANTON NUMBER: US/09/473,551

WUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 96

TYPE: PRT
                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09220528A

Batent No. 6284540

GENERAL INPORMATION:
APPLICANT: Milbrandt, Jeffrey D.
APPLICANT: Baloh, Robert H.
TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor FILE REFERENCE: 6029-798

CURRENT APPLICATION NUMBER: US/09/220,528A

CURRENT FILING DATE: 1998-12-24

EARLIER PILION NUMBER: 60/108,148

EARLIER FILING DATE: 1998-11-22

EARLIER FILING DATE: 1998-01-29

EARLIER FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 120

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 19
US-09-662-183A-35
US-09-220-228-32
US-09-220-238-32
US-09-662-183A-4
US-09-538-092-746
US-09-252-991A-26175
US-09-133-092-746
US-09-143-365A-7
US-09-143-365A-7
US-09-267-177-17
US-09-267-177-17
US-09-267-177-34
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US-09-267-177-34
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US-09-267-177-34
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US-09-513-999C-6280
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US-10-004-860-880
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100.0%; Pred. No. 4;
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Best Local Similarity 100.
Matches 8; Conservative
 TYPE: PRT
CORGANISM: Homo sapiens
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Sequence 6, Appli
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              GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                     May 15, 2006, 09:57:49 ; Search time 27 Seconds
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/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RCOMB.pep:*
/cgn2_6/ptodata/1/iaa/RECOMB.pep:*
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US-09-347-613C-7
US-09-347-613C-12
US-09-662-183A-12
US-09-662-183A-12
US-09-347-613C-11
US-09-347-613C-11
US-09-662-183A-16
US-09-662-183A-16
US-09-662-183A-16
US-09-347-613C-5
US-09-347-613C-5
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NAME/KEY: VARIANT
LOCATION: (108)
1 DOCHER INON: (108)
1 OTHER INCOMATION: Wherein Xaa at position 108 designates Ala or Pro
US-09-347-613C-7
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OTHER INFORMATION: Wherein Xaa at position 107 designates Asn or
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JERGER NO. 0593133

APPLICANT: Johansen, Teit E.

APPLICANT: Blom, Nikolaj

TITLE OF INVENTION: No. 6593133e1 Neurotrophic Factors

FILE REFERENCE: NeuroSearch 19313e2

CURRENT FILING DATE: 1999-07-02

PRIOR PLILOG DATE: 1998-07-05

PRIOR FILING DATE: 1998-07-09

PRIOR PLILOG DATE: 1998-08-19

PRIOR PLILOG DATE: 1998-08-19

PRIOR PLILOG DATE: 1998-08-19

PRIOR PLILOG DATE: 1998-08-19

PRIOR PLILOG DATE: 1998-08-25

PRIOR PLILOG DATE: 1998-08-25

PRIOR PLILOG DATE: 1998-10-05

PRIOR PLILOG DATE: 1998-10-13

PRIOR PLILOG DATE: 1998-10-13

PRIOR PLING DATE: 1998-10-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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1.5%; Score 8; DB 2
Best Local Similarity 100.0%; Pred. No. 4.7
Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Sequence 12, Application US/09347613C; Patent No. 6593133
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 113
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ORGANISM: Homo sapiens
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                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                     FEATURE: NAME/KEY: VARIANT
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US-09-662-183A-7
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LENGTH: 113
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APPLICANT: Milbrandt, Jeffrey D.
APPLICANT: Milbrandt, Joeffrey D.
TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor:
FILE REFERENCE: 6029-798
CURENT APPLICATION NUMBER: US/09/220,528A
CURENT APPLICATION NUMBER: US/218,698
EARLIER APPLICATION NUMBER: 09/218,698
EARLIER FILING DATE: 1998-11-22
EARLIER FILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: 09/163,283
EARLIER APPLICATION NUMBER: 09/163,283
EARLIER APPLICATION NUMBER: 09/163,283
EARLIER FILING DATE: 1998-11-12
SEARLIER FILING DATE: 1998-11-12
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APPLICANT: JOHNSON, Teit E.
APPLICANT: Blom, Nikolaj
APPLICANT: Blom, Nikolaj
APPLICANT: Hansen, Claus
TITLE OF INVENTION: No. 6593133el Neurotrophic Factors
FILE REFERENCE: NeuroSearch 19313-001
CURRENT PAPPLICATION NUMBER: US/09/347, 613C
CURRENT FILING DATE: 1999-07-02
PRIOR PELING DATE: 1998-07-06
PRIOR PELING DATE: 1998-07-09
PRIOR PELING DATE: 1998-08-19
PRIOR PELING DATE: 1998-08-19
PRIOR PELING DATE: 1998-08-25
PRIOR FILING DATE: 1998-10-05
PRIOR PELING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: USSN 60/103,908
PRIOR PELING DATE: 1998-10-05
PRIOR PELING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: DANISH 1998 01265
PRIOR FILING DATE: 1998-10-06
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                                                                                            Query Match 1.5%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 4; Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-220-528-3
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      ; ORGANISM: Homo sapiens
US-09-473-551-9
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PRIOR APPLICATION NUMBER: USSN CV. LO. PRIOR FILING DATE: 1998-10-13
PRIOR PILING DATE: 1998-10-6
PRIOR APPLICATION NUMBER: DANISH 1998 01265
PRIOR APPLICATION NUMBER: 09/347,613
PRIOR FILING DATE: 2000-07-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LEGGH: 113
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Patent No. 6284540
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                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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OTHER INFORMATION: Wherein Xaa at position 108 designates Ala or Pro
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GENERAL NO. 0/34284

APPLICANT: Johansen, Teit E.
APPLICANT: Blom, Nikolaj

APPLICANT: Blom, Nikolaj

APPLICANT: Blom, Nikolaj

APPLICANT: Hansen, Claus

TITLE OF INVENTION: No. 6734284el Neurotrophic Factors

FILE REFERERENCE: 19313-001 DIV

CURRENT APPLICATION NUMBER: US/09/662,183A

CURRENT FILING DATE: 2000-09-14

PRIOR FILING DATE: 1998-07-06

PRIOR FILING DATE: 1998-07-09

PRIOR FILING DATE: 1998-08-19

PRIOR FILING DATE: 1998-08-19

PRIOR FILING DATE: 1998-08-19

PRIOR FILING DATE: 1998-08-19

PRIOR FILING DATE: 1998-08-18

PRIOR FILING DATE: 1998-08-18
                                                                             APPLICANT: Johnnsen, Teit E.
APPLICANT: Blom, Nikolaj
APPLICANT: Blom, Claus
TITLE OF INVENTION: No. 6734284el Neurotrophic Factors
FILE REFERENCE: 19313-001 DIV
CURRENT APLICATION NUMBER: US/09/662,183A
CURRENT FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                    PRIOR APPLICATION WURBER: DANISH 1998 00904
PRIOR FILING DATE: 1998-07-06
PRIOR PELLING DATE: 1998-07-06
PRIOR PELLING DATE: 1998-07-09
PRIOR PELLING DATE: 1998-07-09
PRIOR PELLING DATE: 1998-07-09
PRIOR PELLING DATE: 1998-08-19
PRIOR PELLING DATE: 1998-08-19
PRIOR PELLING DATE: 1998-08-15
PRIOR PELLING DATE: 1998-08-25
PRIOR PELLING DATE: 1998-08-25
PRIOR PELLING DATE: 1998-10-05
PRIOR PELLING DATE: 1998-10-05
PRIOR PELLING DATE: 1998-10-05
PRIOR PELLING DATE: 1998-10-05
PRIOR PELLING DATE: 1998-10-06
PRIOR PELLING DATE: 2000-07-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VOR: 2.1
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100.0%; Pred. No. 4.7;
tive 0; Mismatches
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Sequence 12, Application US/09662183A
Patent No. 6734284
     Sequence 7, Application US/09662183A Patent No. 6734284
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (107)
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LENGTH: 113
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APPLICANT: Milbrandt, Jeffrey D.
APPLICANT: Milbrandt, Jeffrey D.
TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor;
FILE REFERENCE: 6029-7998
CURRENT APPLICATION NUMBER: US/09/220,528A
CURRENT FILING DATE: 1998-12-24
EARLIER PILING DATE: 1998-12-22
EARLIER PILING DATE: 1998-11-12
EARLIER PILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: 09/163,283
EARLIER PILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PatentIn Ver. 2.0
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Sequence 6, Application US/09347613C

Sequence 6, Application US/09347613C

Sequence 6. Application GS 93133

GENERAL INFORMATION:

APPLICANT: Johansen, Teit E.

APPLICANT: Blow, Nikolaj

APPLICANT: Hansen, Claus

TITLE OF INVENTION: No. 6593133el Neurotrophic Factors

FILE REPRENCE: Neurosearch 19313-001

CURRENT REPLICATION NUMBER: US/09/347,613C
                                                                                                  Query Match
1.5%; Score 8; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches
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Pred. No. 4.8;
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1.5%; Score 8; DB 2
Best Local Similarity 100.0%; Pred. No. 4.8
Best Conservative 0; Mismatches
LOCATION: (95)
COTHER INFORMATION: glycosylated asparagine US-09-662-183A-12
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Gaps
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; OTHER INFORMATION: Wherein Xaa at position 111 designates Ala or Pro
US-09-662-183A-6
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OTHER INFORMATION: Wherein Xaa at position 110 designates Asn or Thr
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                                                                                                                             Length 116;
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                                                                                                                                                                                               0; Indels
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GENERAL NO. 0/34204

APPLICANT: Johansen, Teit E.

APPLICANT: Blom, Nikolaj

APPLICANT: Blom, Nikolaj

APPLICANT: Blom, Nikolaj

APPLICANT: Blom, Nikolaj

APPLICANT: Halom, Nikolaj

APPLICANT: Halom, Nikolaj

TITLE OF INVENTION: No. 6/34284el Neurotrophic Factors

TITLE TELERERERENCE: 19313-001 DIV

CURRENT APPLICATION NUMBER: USO0-09-14

PRIOR FILING DATE: 1998-07-09

PRIOR FILING DATE: 1998-07-09

PRIOR FILING DATE: 1998-07-09

PRIOR FILING DATE: 1998-08-19

PRIOR FILING DATE: 1998-08-15

PRIOR FILING DATE: 1998-08-25

PRIOR FILING DATE: 1998-10-05

PRIOR FILING DATE: 1998-10-05

PRIOR FILING DATE: 1998-10-06

PRIOR FILING DATE: 1998-10-13

PRIOR FILING DATE: 1998-10-13

PRIOR FILING DATE: 1998-10-13

PRIOR FILING DATE: 1098-10-13

PRIOR FILING DATE: 2000-07-02

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 6

LENGTH: LENGTH DATE: 2000-07-02

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 6

LENGTH: LENGTH DATE: 2000-07-02

NUMBER OF SEQ ID NOS: 43
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100.0%; Pred. No. 4.8;
tive 0; Mismatches
                                                                                                                          Query Match 1.5%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 4.8; Matches 8; Conservative 0; Mismatches
      i LOCATION: (98)
i OTHER INFORMATION: glycosylated asparagine
US-09-347-613C-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-662-183A-11
; Sequence 11, Application US/09662183A
; Patent No. 6734284
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 6, Application US/09662183A
; Patent No. 6734284
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION: Wherein Xaa at position 110 designates Asn or Thr FEATURE:
NAME/KEY: VARIANT
LOCATION: (111)
OTHER INFORMATION: Wherein Xaa at position 111 designates Ala or Pro US-09-347-613C-6
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US-09-347-613C-11
; Sequence 11, Application US/09347613C
; Patent No. 6593133
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
APPLICANT: Hansen, Claus
; TITLE OF INVENTION: No. 6593133el Neurotrophic Factors
; TILE REFERENCE: NeuroSearch 19313-001
; CURRENT APPLICATION NUMBER: US/09/347,613C
; FRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-05
; PRIOR FILING DATE: 1998-07-09
; PRIOR FILING DATE: 1998-08-19
; PRIOR FILING DATE: 1998-08-25
; PRIOR FILING DATE: 1998-08-25
; PRIOR FILING DATE: 1998-08-25
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 43
; SCOFWARE: PATENTIN VEY: 2.1
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PRIOR APPLICATION NUMBER: DANISH 1998 00904
PRIOR FILING DATE: 1998-07-06
PRIOR PLING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: USSN 60/092,229
PRIOR PLING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-15
PRIOR PLING DATE: 1998-08-15
PRIOR APPLICATION NUMBER: DANISH 1998 01260
PRIOR FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-06
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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NAME/KEY: CARBOHYD
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FEATURE:

92 GALRPPPG 99

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Gaps
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OTHER INFORMATION: Wherein Xaa at position 134 designates Asn or Thr
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US-09-347-613C-5
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                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Johansen, Teit E.
APPLICANT: Blom, Nikolaj
FILE REFERENCE: Neurocsearch 19313el Neurotrophic Factors
FILE REFERENCE: Neurocsearch 19313cl
CURRENT APPLICATION NUMBER: US/09/347,613C
CURRENT FILING DATE: 1999-07-02
PRIOR FILING DATE: 1998-07-06
PRIOR FILING DATE: 1998-07-09
PRIOR PELICATION NUMBER: DANISH 1998 01048
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-13
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APPLICANT: Johansen, Teit E.
APPLICANT: Blom, Nikolaj
APPLICANT: Blom, Nikolaj
APPLICANT: Blom, Nikolaj
APPLICANT: Hansen, Claus
TITLE OF INVENTION: No. 6593133e1 Neurotrophic Factors
TITLE OF INVENTION: No. 6593133e1 Neurotrophic Factors
CURRENT APPLICATION NUMBER: US/09/347,613C
CURRENT FILING DATE: 1999-07-02
PRIOR FILING DATE: 1998-07-06
PRIOR PELING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-19
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                                                                                                                 Sequence 5, Application US/09347613C
Patent No. 6593133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   530 GALRPPPG 537
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                                                                 RESULT 14
US-09-347-613C-5
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APPLICANT: Milbrandt, Jeffrey D.
APPLICANT: Milbrandt, Jeffrey D.
TITLE OF INVENTION: Attention, A No. 6284540el Neurotrophic Factor
FILE REFERENCE: 6029-7998
CURRENT APPLICATION NUMBER: US/09/220,528A
CURRENT FILING DATE: 1998-12-24
EARLIER FILING DATE: 1998-12-22
EARLIER FILING DATE: 1998-11-22
EARLIER FILING DATE: 1998-11-22
EARLIER FILING DATE: 1998-11-12
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 120
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TITLE OF INVENTION: No. 673284el Neurotrophic Factors
FILE REFERENCE: 19313-001 DIV
GURRENT APPLICATION NUMBER: US/09/662,183A
CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: DANISH 1998 00904
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: USSN 60/092,229
PRIOR APPLICATION NUMBER: USSN 60/092,229
PRIOR PILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-19
PRIOR PRILING DATE: 1998-08-25
PRIOR PRILICATION NUMBER: USSN 60/097,774
PRIOR PILING DATE: 1998-10-05
PRIOR PRILING DATE: 1998-10-05
SOGFWARER
PRINCATION NUMBER: 09/347,613
PRIOR FILING DATE: 2000-07-02
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100.0%; Pred. No. 4.8;
tive 0; Mismatches
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CTHER INFORMATION: glycosylated asparagine US-09-662-183A-11
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Patent No. 6284540
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Best Local Similarity 100.
Matches 8; Conservative
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LENGTH: 116
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testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
osteopathic; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antisarthritic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; neural disorder;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; lung;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;
Parkinson's disease; immunological disorder; arthritis; asthma; AlDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular disorders.
                 Adj93383
Adj93387
Adj93388
Adj93388
Adj93378
Adj93372
Adj93382
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Addj93457
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                    ADJ93383
ADJ93388
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ADJ93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ93358 standard; protein; 541 AA
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WPI; 2004-099381/10.
N-PSDB; ADJ93357.
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ADJ93358

ID ADJ93358

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3833.934 Million cell updates/sec
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                    GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Gapop 60.0 , Gapext 60.0
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Match Length DB
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Perfect score:
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This invention relates to a novel testis-specific tubulin tyrosine-ligase

-like polypeptide, designated the BGS-42 polypeptide. The invention may

be useful for the development of compounds with a cytostatic, respiratory

-den, gastrointestinal-den, neuropotective, endocrine-den,

-antinflammatory, anabolic, hypertensive, osteopathic, nootropic,

antinflammatory antiseborrheic or dermatological activity acting as

cyrosine ligase modulators. In addition, the disclosed sequences may be

useful for gene therapy. The BGS-42 polypeptide or polynuclectide can be

useful for diagnosing a pathological condition or a susceptibility to a

pathological condition in a subject, and for preventing, treating or

ameliorating a medical condition, such as a disorder related to aberrant

cubulin ligase activity, aberrant cellular proliferation, reproductive

carboxypeptidase activity, aberrant cellular proliferation, reproductive

disorders, testicular disorders, testicular cancer, pulmonary disorders,

neural disorders, brain cancer, liver cancer, pulmonary disorders,

neural disorders, brain cancer, liver cancer, or proliferative condition

of the testis, lung, small intestine, brain or lymph tissue. The BGS-42

polypeptide, polynucleotide, or their modulators are also useful for

treating infertility, Cushings's syndrome, emphysema, pneumonia, Addison's

disorders including arthritis, asthma, AlDS, sepsis, acne, Sjogren's

classase or scleroderma. The antibodies may be used to purify, detect and

target the BGS-42 polypeptides. The present sequence is that of the human

EGG target the BGS-42 polypeptides. ö ELPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAHPLEPVLRGLKTAEGALRPPPGGKG 540 LINELITSVNPQTDIDGERNIMIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVV 180 240 300 360 DHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWFPSTPVTAQLCAQVQEDTIKVAVD 360 RSCDIGNFELLWRQPVVEPPFFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDAQPLK 420 480 480 ELPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAHPLBPVLRGLKTAEGALRPPFGGKG 540 61 KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQAL 120 121 LNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVV 180 241 AVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQ 300 RSCDIGNFELLWRQPVVEPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDAQPLK 420 1 MASSILKWVVSHQSCSRSSRSRRPDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC 60 1 MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQAL QKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN AVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQ DHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAVD ARGPSAMPDPAQGPPSPALQRDLGLKEEKGLPLALLAPLRGAAESGGAAQPTRTKAAGKV Gaps ; Query Match 100.0%; Score 541; DB 8; Length 541; Best Local Similarity 100.0%; Pred. No. 0; Matches 541; Conservative 0; Mismatches 0; Indels C Claim 5; SEQ ID NO 2; 343pp; English. Seguence 541 AA; 541 ß 481 181 241 301 361 541 61 121 181 301 361 421 421 481 g 셤 ò 셤 셤 ઠે d ò 셤 ò g à g ò ò 유 ò

This invention relates to a novel testis-specific tubulin tyrosine-ligase

- like polypeptide, designated the BGS-42 polypeptide. The invention may

be useful for the development of compounds with a cytostatic, respiratory

- den, gastrointestinal-Gen, neuroprotective, endocrine-Gen,

antiparkinsonian, antiarthritic, antiaschmatic, anti-HIV, antibacterial,

muniosuppressive, antiesborrineic or dermatological activity acting as

cyrosine ligase modulators. In addition, the disclosed sequences may be

useful for gene therapy. The BGS-42 polypeptide or polymuclectide can be

useful for gene therapy. The BGS-42 polypeptide or polymuclectide can be

used for diagnosing a pathological condition or a susceptibility to a

pathological condition in a subject, and for preventing, treating or

ameliorating a medical condition, such as a disorder related to aberrant

cubulin ligase activity, a disorder related to aberrant tubulin
carboxypeptidase activity, and sorders, colon cancer, pulmonary disorders,

carboxypeptidase activity, and sorders, colon cancer, stomach cancer,

carboxypeptidase activity, and disorders, colon cancer, stomach cancer,

carboxypeptidase activity, and disorders, colon cancer, stomach cancer,

carboxypeptidase activity, and sorders, colon cancer, stomach cancer,

carboxypeptidaers, brain cancer, liver cancer, or proliferative condition

of the testis lung, small intestine, brain or lymph tissue. The BGS-42

polypeptide, polymucleotide, or their modulators are also useful for

treating infertility, cushing's syndrome, emphysema, pneumonia, Addison's BGS-42 polypeptide; Cycotatic; respiratory-Gen; gastrointestinal-Gen; neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive; osteopathic; noctropic; antiparkinsonian; antiarthritic; antiasthmatic; anti-HIV, antibacterial; immunosuppressive; antiseborrheic; dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase; tubulin-carboxypeptidase; cellular proliferation; reproductive disorder; testicular disorder; pulmonary disorder; lung cancer; gastrointestinal disorder; concer; pulmonary disorder; brain; proliferative condition; testis; lung; small intestine; brain; lymph tissue; infertility; Cushing's syndrome; emphysema; brain; lymph tissue; infertility; Cushing's syndrome; parkinson's disease; acromegaly; Alzheimer's disease; parkinson's disease; arthritis; asthma; ADS; New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, e.g. aberrant cellular proliferation, reproductive disorders or testicular Human tubulin tyrosine ligase protein consensus sequence SeqID13. testis-specific tubulin tyrosine-ligase-like polypeptide; sepsis; acne; Sjogren's disease; scleroderma; human. Example 4; SEQ ID NO 13; 343pp; English. ADJ93365 standard; protein; 541 AA. (BRIM) BRISTOL-MYERS SQUIBB CO. 09-JUL-2003; 2003WO-US021605. 09-JUL-2002; 2002US-0394725P. Nelson TC; (first entry) WPI; 2004-099381/10. Wu S, N-PSDB; ADJ93364 WO2004005487-A2. 541 Homo sapiens 15-JAN-2004. 541 S Feder JN, disorders. Synthetic. ADJ93365; RESULT 2 ADJ93365

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BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
BGS-42 polypeptide; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermacological; tyrosine ligase modulacor; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; lung;
small intestine; brain; lymph tissue; acromegaly; Alzheimer's disease;
emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARGPSAMPDPAQGPPSPALQRDLGLKEEKGLPLALLAPLRGAAESGGAAQPTRTKAAGKV 480
            -42 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of the tubulin tyrosine ligase protein consensus sequence which was used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                       1 MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC
                                                                                                                                                                                                                                                                                                                                                                         KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQAL
                                                                                                                                                                                                                                                                                                1 MASSILKWVVSHQSCSRSSRSKPRDQREFAGSSDLSSRQDAENAEAKLRGLFGQLVDIAC
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                                                                                                                                                                                                                                   Gaps
  disease, acromegaly, Alzheimer's disease, or Parkinson's disease.
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                                                                                                                                                                                            Length 541;
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                                                                                                                                                                                          95.0%; Score 514; DB 8;
100.0%; Pred. No. 0;
ive 0; Mismatches 0
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Matches 514; Conservative
                                                                                                                                                        Sequence 541 AA;
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This invention relates to a novel testis-specific tubulin tyrosine-ligase convention, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory conventional designated the BGS-42 polypeptide. The invention may assistant designations and the compounds with a cytostatic, respiratory contine-fan, antiarchritic, antiaschmatic, antiabacterial, antiarchristic, antiaschmatic, antiabacterial, conting antiabacterial activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be used for diagnosing a pathological condition or a susceptibility to a cytosine ligase modulators. In addition, the disclosed sequences may be used for diagnosing a pathological condition or a susceptibility to a cytosine ligase activity, addisorder condition or a susceptibility to a meliorating a medical condition, such as a disorder related to aberrant tubulin ligase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders testicular cancer, pulmonary disorders, lung cancer, gastrointestinal disorders, colon cancer, pulmonary disorders, lung cancer, lung cancer, lung cancer, lung cancer, lung cancer, lung small intestine, brain or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsies, acromegaly, Alzheimer's disease, or Parkinson's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of the TILI domain of the human BGS-42 protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                              testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, inl for preventing, treating or ameliorating a medical condition, errant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Parkinson's disease; immunological disorder; arthritis; asthma; AIDS; sepsis; acne; Sjogren's disease; scleroderma; human; TTL1 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 14; 343pp; English.
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                                                                                                                                                                                                                       09-JUL-2002; 2002US-0394725P.
                                                                                                                                                                                                                                                              (BRIM ) BRISTOL-MYERS SQUIBB
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Best Local Similarity 100.0
Matches 293; Conservative
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                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                       useful for
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                                                                                                                                                                                                                                                                               KW BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen; BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen; meuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive; w osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic; anti-HIV, antibacterial; immunosuppressive; antischorrheit; dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase; tubulin-carboxypeptidase; cellular proliferation; reproductive disorder; w tubulin-carboxypeptidase; cellular proliferation; reproductive disorder; w pastrointestinal disorder; colon cancer; pulmonary disorder; lung cancer; w brain cancer; not cancer; proliferative condition; testis; lung; brain; lymph tissue; infertility; dushing's syndrome; emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease; w Parkinson's disease; immunological disorder; archritis; asthma; AIDS; w sepsis; acne; Sjogren's disease; scleroderma; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antinflammatory, anabolic, hypertensive, osteopathic, nootropic, antinflammatory, anabolic, hypertensive, osteopathic, nootropic, antinflammatory, antiathritic, antiasthmatic, anti-HIV, antibacterial, immunosuppressive, antiaeborrheic or dermacological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be used for diagnosing a pathological condition a susceptible or polynucleotide can be used for diagnosing a pathological condition or a susceptibility to a pathological condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin ligase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders, testicular disorders, testicular disorders, testicular disorders, colon cancer, pulmonary disorders, lung cancer, gastrointestinal disorders, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a novel testis-specific tubulin tyrosine-ligase-like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory
181 SPLLPAHNMWISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, e.g. aberrant cellular proliferation, reproductive disorders or testicular
                                                 241 YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDI 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 4; 343pp; English.
                                                                                                                                                                                                                                                        Human BGS-42 protein sequence SeqID4.
                                                                                                                                                   ADJ93360 standard; protein; 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BRIM ) BRISTOL-MYERS SQUIBB CO.
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                                                                                                                                                                                                                      (first entry)
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                     treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS -42 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AlDS, sepsis, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of the human
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD 60
                                                                                                                                                                                                                                                                                                                                                                                               133 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
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polynucleotide, or their modulators are also useful for
                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                       Length 242;
                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                     BGS-42 protein (partial sequence) of the invention
                                                                                                                                                                                                                                                                                       44.7%; Score 242; DB 8; Le
100.0%; Pred. No. 1.7e-252;
iive 0; Mismatches 0;
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02-MAY-2003; 2003US-0467139P.
02-MAY-2003; 2003US-0467230P.
19-MAY-2003; 2003US-0471306P.
19-MAY-2003; 2003US-0471336P.
08-JUL-2003; 2003US-0485223P.
08-JUL-2003; 2003US-0486446P.
14-JUL-2003; 2003US-0486480P.
08-MG-2003; 2003US-0486480P.
08-AUG-2003; 2003US-0493577P.
08-SEP-2003; 2003US-0493577P.
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                                                                                                                                                                                                                                                                                                                                           242; Conservative
                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                         Sequence 242 AA;
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     polypeptide,
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                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                              Matches
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(FIVE-) FIVE PRIME THERAPEUTICS INC

Williams LT; Masuoka L, Chu K, Hestir K, Lee E,

WPI; 2004-775861/76.

N-PSDB; ADU02015.

New first nucleic acid molecule comprising a polynucleotide sequence given in the specification, useful in preparing a composition for diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.

Claim 14; SEQ ID NO 1214; 291pp; English.

The invention describes a new first nucleic acid molecule comprising a polynucleotide sequence given in the specification. Also described are: an animal injected with the nucleic acid molecule; a second nucleic acid molecule; a second nucleic acid molecule or described are: an animal injected with the nucleic acid molecule or that hybridises to the first polynucleotide sequence that drives the expression of the nucleic acid molecule and a promocer that drives the expression of the nucleic acid molecule; a control of the nucleic acid molecule; a nucleic acid molecule; a nucleic acid composition comprising the nucleic acid molecule; a by the compression of the nucleic acid molecule; a control or nore compositions comprising the nucleic acid molecule; a nucleic acid composition comprising the polypeptide; a polypeptide or nucleic acid molecule; a nucleic acid molecule; and core sumposition comprising the polypeptide and a carrier or buffer; a cell animal injected with the polypeptide; a polypeptide composition comprising the polypeptide molecule and a carrier or buffer; a cell comprising the polypeptide molecule and a carrier or buffer; a cell comprising the polypeptide molecule and a carrier or buffer; a cell comprising the polypeptide molecule or title cransduced, or infected molecule of the nucleic acid molecule or its comprising a perioe of the nucleic acid molecule or its comprising the presence of the nucleic acid molecule or its complement; determining the presence of the nucleic acid molecule or its composition or crystal structure; jamunishing a hording specifically recognising, binding to or modulating the barerning the presence of the nucleic acid molecule or its biological activity of at least one polypeptide encoded by a nucleic acid molecule or its biological activity of at least one polypeptide encoded by a nucleic acid molecule or its biological activity of a least one polypeptide and a carrier; a bacteriophage, where the antibody is diagnosing a disease, disorder, syndreminally active anibody comp invention.

Sequence 402 AA;

ö Gaps ; 0 Length 402; Indels . 0 18.7%; Score 101; DB 8; I 100.0%; Pred. No. 1.2e-99; ive 0; Mismatches 0; Best Local Similarity 100. Matches 101; Conservative Query Match

1 MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC 60

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KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLV 101 61

361 KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLV 401

testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; neural disorder;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; lung;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
parkinson's disease; immunological disorder; arthritis; asthma; ADS; sepsis; acne; Sjogren's disease; scleroderma; human. Human BGS-42 protein peptide fragment SeqID21. ADJ93373 standard; peptide; 49 AA. 06-MAY-2004 (first entry) Homo sapiens. ADJ93373; RESULT 6 4DJ93373

WO2004005487-A2.

15-JAN-2004.

09-JUL-2003; 2003WO-US021605.

09-JUL-2002; 2002US-0394725P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Wu S, Nelson TC; Feder JN,

WPI; 2004-099381/10.

e.g. New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular disorders.

Disclosure; SEQ ID NO 21; 343pp; English.

This invention relates to a novel testis-specific tubulin tyrosine-ligase

"Ike polypeptide, designated the BGS-42 polypeptide. The invention may

be useful for the development of compounds with a cytostatic, respiratory

"Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,

"antinflammatory, anabolic, hypertensive, osteopathic, nootropic,

antinflammatory, anabolic, hypertensive, osteopathic, nootropic,

antinflammatory, anabolic, antiasthmatic, antiabacterial,

immunosuppressive, antiasborrheic or dermatological activity acting as

tyrosine ligase modulators. In addition, the disclosed sequences may be

tyrosine ligase modulators. In addition, the disclosed sequences may be

conseful for gene therapy. The BGS-42 polypeptide or polynucleotide can be

useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be

useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be

consecultion in a subject, and for preventing, treating or

maliorating a medical condition, such as a disorder related to aberrant

tubulin ligase activity, a disorder related to aberrant tubulin
carboxypeptidase activity, a berrant cellular proliferation, reproductive

clasorders, testicular disorders, testicular cancer, stomach cancer,

lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,

clasorders polymucleotide, or their modulators are also useful for

treating infertility, Cushimer's disease, or parkinson's disease. The BGS
creating infertility, Cushimer's disease, or Parkinson's disease. The BGS
creating including arthritis, asthma, ALDS, sepsis, acne, Sjogren's

disease or scleroderma. The antibodies may be used to purify, detect and

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                    ADJ93452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel testis-specific tubulin tyrosine-ligase-like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory-Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antiatinal-Gen, antiathritic, antiathmatic, notropic, antiparkinsonian, antiathritic, antiathmatic, anti-HIV, antibacterial, immunosuppressive, antiseborrheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polynuclectide can be used for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, and for preventing, treating or
                                                                                                                                                                                                                                                                                                                                      BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen; neuroprotective; endocrine-Gen; antinflammatory; anabolic; hypertensive; osteopathic; nootropic; antiparkinsonian; antiathritic; antiasthmatic; antibacterial; immunosuppressive; antiseborrheic; dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase; tubulin-carboxypeptidase; cellular proliferation; reproductive disorder; testicular cancer; pulmonary disorder; lung cancer; gastrointestinal disorder; condicative condition; testis; lung; brain cancer; liver cancer; proliferative condition; testis; lung; manl intestine; brain; lymph tissue; infertility; Oushing's syndrome; emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease; Parkinson's disease; scleroderma; human.
target the BGS-42 polypeptides. The present sequence is that of a peptide fragment of the human BGS-42 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                             Gaps
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                                                                                                                      192 DTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN 240
                                                                                                                                     DIKEDIROWFLVIDWNPLIIWFYKESYLRFSIORFSLDKLDSAIHLCNN 49
                                                                                                                                                                                                                                                                                                                              testis-specific tubulin tyrosine-ligase-like polypeptide;
                                                                 Length 49;
                                                                                          0; Indels
                                                                  DB 8; Le
3.1e-44;
                                                                                                                                                                                                                                                                                                   Human BGS-42 protein peptide fragment SeqID24.
                                                    9.1%; Scort No. -..
100.0%; Pred. No. -..
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, SEQ ID NO 24; 343pp; English.
                                                                                                                                                                                                                  ADJ93376 standard; peptide; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39-JUL-2003; 2003WO-US021605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUL-2002; 2002US-0394725P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feder JN, Wu S, Nelson TC;
                                                                                                                                                                                                                                                                        (first entry)
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-099381/10.
                                                            Query Match
Best Local Similarity
Marches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MO2004005487-A2
                                       Sequence 49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                        06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders
                                                                                                                                                                                                                                               ADJ93376;
                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                         ADJ93376
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c ameliorating a medical condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin-car carboxypeptidase activity, aderrant cellular proliferation, reproductive disorders, testicular disorders, testicular disorders, colon cancer, pulmonary disorders, con entral disorders, brain cancer, liver cancer, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide, polymucleotide, or their modulators are also useful for creating infertility, Cushing's syndrome, emphysema, pheumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-72 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of a peptide fragment of the human BGS-42 protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen; neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive; osteogathic; noctropic; antiparkinsonian; antiarthritic; antiasthmatic; anti-lacterial; immunosuppressive; antiseborrheic; dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase; tubulin-carboxypeptidase; cellular proliferation; reproductive disorder; testicular disorder; testicular dancer; proliferation; reproductive disorder; pastrointestinal disorder; colon cancer; promach cancer; neural disorder; brain cancer; proliferative condition; testis; lung; small intestine; brain; lymph tissue; infertility; Cushing's syndrome; emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease; Parkinson's disease; immunological disorder; arthritis; asthma; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sepsis; acne; Sjogren's disease; scleroderma; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 482 LPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAHPLEPVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human BGS-42 protein-related protein sequence #103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.8%; Score 42; DB 8; Local Similarity 100.0%; Pred. No. 1e-36; les 42; Conservative 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ93452 standard; protein; 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-2002; 2002US-0394725P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-099381/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42 AA;
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Centinitlammatory, anabolic, hypertensive, endocrine-Gen, dastrinitlammatory, anabolic, hypertensive, esteopathic, nootropic, antiinflammatory, anabolic, hypertensive, osteopathic, nootropic, antiinflammatory, anabolic, hypertensive, osteopathic, nootropic, antiinflammatory, anabolic, hypertensive, osteopathic, nootropic, contiparkinsonian, antiseborrheic or deracological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polymoleotide can be used for diagnosing a pathological condition or a susceptibility to a pathological condition or a susceptibility to a complex condition in a subject, and for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant cubulin ligase activity, a disorder related to aberrant tubulin-carboxypeptidase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders, testicular disorders, comer, pulmonary disorders, lung amedical disorders, prain cancer, pathological cancer, polymetriestinal disorders, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polymetride, polymetricotide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The astrinity, astrinity, asthma, AlDS, sepsis, acro, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 protein of the invention.
                                                                                                                         This invention relates to a novel testis-specific tubulin tyrosine-ligase -like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory
Disclosure; Fig 7B; 343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 61 AA;
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DB 8; Length 61; 2.6e-33; 0, Indels 1 MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQ 39 1 MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQ 39 Query Match 7.2%; Score 39; DB Best Local Similarity 100.0%; Pred. No. 2.6 Matches 39; Conservative 0; Mismatches ð

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Gaps ö

> ADJ93374 standard; peptide; 26 AA 06-MAY-2004 (first entry) ADJ93374; ADJ93374 셤

testis-specific tubulin tyrosine-ligase-like polypeptide; Human BGS-42 protein peptide fragment SeqID22.

BGS-42 polypeptide, cytostatics, respiratory-Gen; gastrointestinal-Gen; neuroprotective; endocrine-Gen; antinflammatory; anabolic; hypertensive; osteopathic; nocropic; antiparkinsonian; antiarthritic; antiasthmatic; anti-parkinsonian; antiarthritic; antiasthmatic; anti-parkinsonian; antiarthritic; antiasthmatic; dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase; tubulin-carboxypeptidase; cellular proliferation; reproductive disorder; testicular disorder; testicular cancer; pulmonary disorder; neural disorder; gastrointestinal disorder; colon cancer; ptomach cancer; neural disorder; small intestine; brain; lymph tissue; infertility; Cushing's syndrome; emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease; Parkinson's disease; mmunological disorder; atthritis; asthma; AlDS; sepsis; acne; Sjogren's disease; scleroderma; human.

Homo sapiens

WO2004005487-A2

.5-JAN-2004.

09-JUL-2003; 2003WO-US021605

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This invention relates to a novel testis-specific tubulin tyrosine-ligase clear in the polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory. Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, dantializathmitic, antiasthmic, antibacterial, antiathmitic, antibacterial, immunosuppressive, antiaeborrheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be cused for diagnosing a pathological condition or a susceptibility to a pathological condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin carboxypeptidase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders, testicular disorders, colon cancer, stomach cancer, converse in cancer, interestinal disorders, stomach cancer, converse in the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide, polymeptide, polymeptide can be used as a preventive amphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS converse in the used as a preventive agent for immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen; neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive; osteogethic; nocropic; antiparkinsonian; antiarthritic; antiasthmatic; anti-matchic; nocropic; antiparkinsonian; antistrhitic; antibacterial; immunosuppressive; antiseborrhaic; dermatclogical; tyrosine ligase modulator; gene therapy; tubulin ligase; tubulin-carboxypeptidase; cellular proliferation; reproductive disorder; testicular disorder; testicular cancer; pulmonary disorder; lung cancer; gastrointestinal disorder; concer; stomach cancer; neural disorder; brain cancer; liver cancer; proliferative condition; testis; lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of a peptide fragment of the human BGS-42 protein of the invention.
                                                                                                                                                                                                        e.g.
                                                                                                                                                                              New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
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100.0%; Pred. No. 1.4e-19;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 22; 343pp; English.
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                                          (BRIM ) BRISTOL-MYERS SQUIBB CO.
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09-JUL-2002; 2002US-0394725P.
                                                                                        Wu S, Nelson TC,
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                                                                                                                                   WPI; 2004-099381/10.
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Best Local Similarity
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                                                                                                                                                                                                                                                     disorders.
                                                                                        Feder JN,
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This invention relates to a novel testis-specific tubulin tyrosine-ligase—
like polypeptide, designated the BGS-42 polypeptide. The invention may
be useful for the development of compounds with a cytostatic, respiratory
Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen
antinflammatory, anabolic, hypertensive, osteopathic, nociropic,
antinflammatory, anabolic, hypertensive, osteopathic, nociropic,
antinflammatory in antiarthritic, antiasthmatic, anti-HIV, antibacterial,
immunosuppressive, antiseborrheic or dermatological activity acting as
tyrosine ligase modulators. In addition, the disclosed sequences may be
useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be
useful for disponsing a pathological condition or a susceptibility to a
pathological condition in a subject, and for preventing, treating or
cused for disponsing a pathological condition, such as a disorder related to aberrant
cubulin ligase activity, aberrant cellular proliferation, reproductive
disorders, testicular disorders, testicular cancer, pulmonary disorders,
carboxypeptidase activity, aberrant cellular proliferation, reproductive
disorders, testicular disorders, testicular cancer, pulmonary disorders,
lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,
neural disorders brain cancer, liver cancer, or proliferative condition
of the testis, lung, small intestine, brain or lymph tissue. The BGS-42
polypeptide, polynucleotide, or their modulators are also useful for
treating infertulity, Cushing's syndrone, emphysema, preumonia, Addison's
disease, arromegaly, Alzheimer's disease, or Parkinson's disease.
Ctreating infertulity, Alzheimer's disease, or Parkinson's disease.
Ctreating infertulity, asthma, AlDS, sepsis, acne, Sjogren's
disease or scleroderma. The antibodies may be used to purify, detect and
ctarget the BGS-42 polypeptides. The present sequence is that of a peptide
ctarget the BGS-42 protein of the invention.
small intestine; brain; lymph tissue; infertility; Cushing's syndrome; emphysema; preumonia; Addison's disease; acromegally; Alzhelmer's disease; Parkinson's disease; immunological disorder; arthritis; asthma; AlDS; sepsis; acne; Sjogren's disease; scleroderma; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-2003; 2003WO-US021605.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feder JN, Wu S, Nelson TC;
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                                                                                                                                                                                                                                                                                                        Homo sapiens.
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ö Gaps . 0 Length 23; 0; Indels Score 23; DB 8; Le Pred. No. 2.1e-16; Mismatches 138 NIWIIKPAAKSRGRDIVCMDRVE 160 4.3%; Scor. 100.0%; Pred 0; M Query Match
Best Local Similarity luv..
Best Z3; Conservative

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1 NIWIIKPAAKSRGRDIVCMDRVE 23
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ADJ93377 standard; peptide; 17 AA. ADJ93377; ADJ93377

RESULT 11

06-MAY-2004 (first entry)

Human BGS-42 protein peptide fragment SegID25

dermatological, tyrosine ligase modulator; gene therapy; tubulin ligase; dermatological, tyrosine ligase modulator; gene therapy; tubulin ligase; tubulin-carboxypeptidase; cellular proliferation; reproductive disorder; testicular disorder; pulmonary disorder; lung cancer; gastrointestinal disorder; colon cancer; stomach cancer; neural disorder; brain cancer; proliferative condition; testis; lung; small intestine; brain, lymph tissue; infertility, Cushing's syndrome; emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease; sepsis; acne; Sjogren's disease; scleroderma; human. BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen; neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic; testis-specific tubulin tyrosine-ligase-like polypeptide;

Homo sapiens

WO2004005487-A2.

15-JAN-2004.

e.g.

09-JUL-2003; 2003WO-US021605.

09-JUL-2002; 2002US-0394725P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Wu S, Nelson TC;

Feder JN,

WPI; 2004-099381/10.

е. 9. New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular disorders.

Disclosure; SEQ ID NO 25; 343pp; English.

This invention relates to a novel testis-specific tubulin tyrosine-ligase compared the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory den useful for the development of compounds with a cytostatic, respiratory gratrointestinal-Gen, neuroprotective, endocrine-Gen, respiratory antiparkinsonian, antiathritic, antiaschmatic, anti-HIV, antibacterial, antiparkinsonian, antiathritic, antiaschmatic, anti-HIV, antibacterial, comminosuppressive, antiseborrheic or dernatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be useful for disponsing a pathological condition, the disclosed sequences may be useful for disponsing a pathological condition, such as a disorder related to aberrant tubulin ligase activity, aberrant cellular proliferation, reproductive carboxypeptidase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders, resticular cancer, pulmonary disorders, certicular disorders, resticular cancer, pulmonary disorders, lung cancer, gastrointestinal disorders, colon cancer, promised alsorders, bulmonary disorders, colon cancer, stomach cancer, neural disorders, brain cancer, inver cancer, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide can be used as a preventive agent for immunological ciscoarders including arthritis, asthma, AIDS, sepsis, acromegaly, Alahaimer's disease, or Parkinson's disease, or Parkinding arthritis, asthma, AIDS, sepsis, acre, signers and enged as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsis, acre, signers and enget and enget and enget the BGS-42 polypeptides. The present sequence is that of a peptide traget the BGS-42 protein of the invention.

Sequence 17 AA;

Gaps . 0 3.1%; Score 17; DB 8; Length 17; 100.0%; Pred. No. 5e-10; ive 0; Mismatches 0; Indels Ouery Match
Best Local Similarity 100.0

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This invention relates to a novel testis-specific tubulin tyrosine-ligase

"Ike polypeptide, designated the BGS-42 polypeptide. The invention may
be useful for the development of compounds with a cytostatic, respiratory
den, gastrointestinal-Gen, neuroprotective, endocrine-Gen,
antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,
antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,
immunosuppressive, antiseborrheic or dematological activity acting as
tyrosine ligase modulators. In addition, the disclosed sequences may be
useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be
useful for diagnosing a pathological condition or a susceptibility to a
cused for diagnosing a pathological condition or a susceptibility to a
pathological condition in a subject, and for preventing, treating or
ameliorating a medical condition, such as a disorder related to aberrant
cubulin ligase activity, aberrant cellular proliferation, reproductive
disorders, testicular disorders, testicular cancer, pulmonary disorders,
carboxypeptidase activity, aberrant cellular proliferation, reproductive
disorders, brain cancer, inver cancer, pulmonary disorders,
che testis, lung, small intestine, brain or lymph tissue. The BGS-42
polypeptide, polynucleotide, or their modulators are also useful for
                                                                                                                                                                                                                                                                                                                                                    testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiathmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; colon cancer; pulmonary disorder; lung cancer;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; lung;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease, acromeagly; Allseimer's disease;
Parkinson's disease; immunological disorder; arthritis; athma; AlDS;
sepsis; acne; Sjogren's disease; scleroderma; human; N-myristoylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                               Human BGS-42 protein-related N-myristoylation peptide SegID47,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 47; 343pp; English.
                                                                                                                                                                ADJ93397 standard; peptide; 16 AA.
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  LKTAEGALRPPPGGKGS 541
                                1 LKTAEGALRPPPGGKGS 17
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                                                                                                                                                                                                                                                               (first entry)
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              disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS -42 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AlDS, sepsis, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of a peptide which represents a site of N-myristoylation in the human BGS-42 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           testis-specific tubulin tyrosine-ligase-like polypeptide;
bGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiathmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; colon cancer; pulmonary disorder; lung cancer;
brain cancer; liver cancer; colon cancer; stomach cancer; neural disorder;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
parkinson's disease; immunological disorder; arthritis; asthma; AIDS;
sepsis; acne; Sjogren's disease; scleroderma; human; N-myristoylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a novel testis-specific tubulin tyrosine-ligase -like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory -Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antiinflammatory, anabolic, hypertensive, osteopathic, nootropic,
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treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human BGS-42 protein-related N-myristoylation peptide SeqID48.
                                                                                                                                                                                                                   Length 16;
                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                 Score 16; DB 8; Li
Pred. No. 5.8e-09;
                                                                                                                                                                                                                            100.0%; Pred. ...
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ93398 standard; peptide; 16 AA.
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                                                                                                                                                                                                                                                                                                379 PPPFSGSDLCVAGVSV 394
                                                                                                                                                                                                                                                                                                                     1 PPPFSGSDLCVAGVSV 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wu S, Nelson TC;
                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-2004 (first entry)
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                                                                                                                                    of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004005487-A2
                                                                                                                                                                              Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
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immunosuppressive, antiseborrheic our dermatcological activity acting as uscripturessive, antiseborrheic our dermatcological activity acting as uscella igase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be used for diagnosing a pathological condition in a subject, and for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin cancer, gastrointestinal disorders, colon cancer, pulmonary disorders, lung cancer, gastrointestinal disorders, colon cancer, stomach cancer, neural disorders, brain cancer, liver cancer, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide, polynucleotide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-42 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of a peptide target the BGS-42 polypeptides. The present sequence is that of a peptide target the BGS-42 polypeptides. The present sequence is that of a peptide target the BGS-42 polypeptides. The present sequence is that of a peptide the barrent and the present sequence is that of a peptide the present sequence is that of a peptide to the present sequence is that of a peptide to the present sequence is that of a peptide to the present sequence is the present sequence is the present of the present sequence is the present s
antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,
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3.0%; Score 16; DB 8; Length 16; 100.0%; Pred. No. 5.8e-09; ive 0; Mismatches 0; Indels 445 LKEEKGLPLALLAPLR 460 1 LKEEKGLPLALLAPLR 16 Query Match Best Local Similarity 100.' Matches 16; Conservative Sequence 16 AA; ò 요

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Gaps .; 0

> ADJ93401 standard; peptide; 16 AA. (first entry) 06-MAY-2004 ADJ93401; RESULT 14 ADJ93401

testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiathmatic;
dermatological; tyrosine ligask modilator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; colon cancer; pulmonary disorder; lung cancer;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; lung;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease, acromegaly; Alzheimer's disease;
parkinson's disease; immunological disorder; arthritis; asthma; AIDS;
sepsis; acne; Sjogren's disease; scleroderma; human; N-myristoylation. Human BGS-42 protein-related N-myristoylation peptide SeqID51.

Homo sapiens

MO2004005487-A2.

15-JAN-2004.

09-JUL-2003; 2003WO-US021605

09-JUL-2002; 2002US-0394725P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Nelson TC; Feder JN, Wu S,

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This invention relates to a novel testis-specific tubulin tyrosine-ligase
-like polypeptide, designated the BGS-42 polypeptide. The invention may
be useful for the development of compounds with a cytostatic, respiratory
ce used for the development of compounds with a cytostatic, respiratory
antinflammatory, anabolic, hypertensive, endocrine-Gen,
antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,
antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,
antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,
converted in addition, the disclosed sequences may be
tyrosine ligase modulators. In addition, the disclosed sequences may be
cused for diagnosing a pathological condition or a susceptibility to a
pathological condition, such as a disorder related to aberrant
cubulin ligase activity, aberrant cellular proliferation, reproductive
cubulin ligase activity, aberrant cellular proliferation, reproductive
disorders, testicular disorders, colon cancer, pulmonary disorders,
lung cancer, gastrointestinal disorders, colon cancer, pulmonary disorders,
colon cancer, proliferation of the testis, lung, small intestine, brain or lymph tissue. The BGS-42
polypeptide, polymucleotide, or their modulators are also useful for
treating infertility, Cushings syndrome, emphysema, pneumonia, Addison's
disorders including arthritis, asthma, AIDS, sepsis, acromegaly, Alzheimer's disease, or Parkinson's disease or scleroderma. The antibodies may be used to purify, detect and
target the BGS-42 polypeptides. The present sequence is that of a peptide
target the BGS-42 prolypeptides. The present sequence is that of a peptide
the region of the present sequence is that of a peptide
                                                                                   e.g.
                                                                                useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                        New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide,
                                                                                                                                                                                                     Disclosure; SEQ ID NO 51; 343pp; English.
WPI; 2004-099381/10.
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Sequence 16 AA;

Gaps ö Length 16; 0; Indels 3.0%; Score 16; DB 8; Le 100.0%; Pred. No. 5.8e-09; 100.0%; Pred. No. 5.0 Live 0; Mismatches 16; Conservative Local Similarity Query Match Matches

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ADJ93396 standard; peptide; 16 AA. (first entry) 06-MAY-2004 ADJ93396; RESULT 15 ADJ93396

Human BGS-42 protein-related N-myristoylation peptide SeqID46.

testis-specific tubulin tyrosine-ligase-like polypeptide;

W BGS-42 polypeptide; cytostatic; respiratory/Gen; gastrointestinal-Gen;

BGS-42 polypeptide; cytostatic; respiratory/Gen; gastrointestinal-Gen;

M reuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;

W steopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;

W dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;

tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;

W gastrointestinal disorder; colon cancer; pulmonary disorder; lung cancer;

M gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;

M small intestine; brain; lymph tissue; infertility; Cushing; syndrome;

R minysema; pneumonia; Addison's disease; arronegaly; Alzheimer's disease;

R parkinson's disease; immunological disorder; arthritis; asthma; AlDS;

M sepsis; acne; Sjogren's disease; scleroderma; human; N-myristoylation.

Homo sapiens.

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This invention relates to a novel testis-specific tubulin tyrosine-ligase composed to the development of compounds with a cytostatic, respiratory be useful for the development of compounds with a cytostatic, respiratory. Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, respiratory antiniflammatory, anabolic, hypertensive, osteopathic, noctropic, antiniflammatory, anabolic, hypertensive, osteopathic, noctropic, antinesuppressive, antiseborrheic or dematological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be useful for disponent a subject, and for preventing, treating or pathological condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin ligase activity, a berrant cellular proliferation, reproductive disorders, testicular disorders, testicular, proliferation, reproductive of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide can be used as a preventive agent for immunological cisorders including arthritis, asthma, AlDS, sepsie, acromegaly, Alzhaimer's disease, or Parkinson's disease. The disease or scleroderma. The antibodies may be used to purify, detect and cisorer and site of N-myristoylation in the human BGS-42 protein of the brease.
                                                                                                                                                                                                                                                                                                                                                                                          New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, e.g. aberrant cellular proliferation, reproductive disorders or testicular
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                                                                                                                                                                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                           09-JUL-2002; 2002US-0394725P
                                                                                                                                            09-JUL-2003; 2003WO-US021605
                                                                                                                                                                                                                                                                                               Feder JN, Wu S, Nelson TC;
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                                            WO2004005487-A2.
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                                                                                             15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders.
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272 QRQGRGAVWGSVIYPS 287 1 QRQGRGAVWGSVIYPS 16 g ò

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Gaps ;

Query Match 3.0%; Score 16; DB 8; Length 16; Best Local Similarity 100.0%; Pred. No. 5.8e-09; Matches 16; Conservative 0; Mismatches 0; Indels

Search completed: May 15, 2006, 09:57:38 Job time : 63 secs THIS PAGE BLANK (USPTO)